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OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 04:44:13 ; Search time 2105.28 seconds

(without alignments)
22709.011 Million cell updates/sec

Title: US-09-677-752-1

Sequence: 1 atgaaaaaacgttttctt.....aaatgcctgcgattctag 2898

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 147140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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36: em_hlg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	2777.8	95.9	2934	6	AX155940
4	1599.4	55.2	14482	1	AE002293
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6	136.4	4.7	12083	1	AE001631
7	136.4	4.7	30656	1	AE002546
8	124.2	4.3	10236	1	AE002189
9	56.6	2.0	14482	1	AE002293
10	48.4	1.7	2949	6	AX155927
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12	47.2	1.6	298283	3	AE003782
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36	41.6	1.4	10029	1	AE006573
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 171 from Patent WO0140474.
ACCESSION AX155928
VERSION AX155928.1 GI:14537033
KEYWORDS
SOURCE
ORGANISM
Chlamydia sp.
Chlamydia sp.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE
1 (bases 1 to 2895)
Probst,P., Bhatia,A., Skeiky,Y.A., Flinn,S.P. and Schollier,J.
AUTHORS
Compounds and methods for treatment and diagnosis of chlamydial
TITLE
infection
JOURNAL
Patent: WO 0140474-A 171 07-JUN-2001;
CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
1..2895
/organism="Chlamydia sp."
/db_xref="taxon:35827"

PAT 22-JUN-2001

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Db	2098	ATGATG GTTTACCAAAATCTCTCGAAGAAATTCATCTGTGATTCCATATCGCTTCCGGA	2157
Qy	2161	tactctcgagggtgtatagcaaggcagaacacaccttctcatatgaaattcagtcaagcc	2220
Db	2158	TACTCTCGGGGATGATAGCAGGGCAGACACACCTTCTCTCTTTAAATTAGTCAGACGC	2217
Qy	2221	tacaccaaatccatgtagcggtttacgcgaaaaaaacacgitatctctctaaaaattactatgc	2280
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Qy	2281	caaggagaaatgctcttcttcatttgcaagaagtttcttgctbctactaaattagttgggctt	2340
Db	2278	CAAGGAAATAATGCTCTTCTTCATTGCAAGAGGTTTCTTGCTACTAAATTAGTTGGGCTT	2337
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Qy	2521	agccctgtctacttactatggtgtggagcctalcgcgcgaagcttcttcaagaagctct	2580
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Qy	2641	ccctaaagcctggagctgtagaatttggcatccaaacccgctctctatagacaagaacaaagg	2700
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LOCUS	AE001360/c	AE001360	14177 bp	DNA	BCF	30-OCT-2000
DEFINITION		Chlamydia trachomatis	section 87	of 87	of the complete genome	
ACCESSION		AE001360	AE001273			
VERSION		AE001360.1	GI:3529342			
KEYWORDS						
SOURCE						
ORGANISM						
		Chlamydia trachomatis.				
		Bacteria: Chlamydiales; Chlamydiaceae: Chlamydia.				
REFERENCE		1 (bases 1 to 14177)				
AUTHORS		Stephens, R.S., Kaimo, S., Lammel, C.J., Fan, J., Marathe, R.,				
		Aravind, L., Mitchell, W.P., Ollinger, L., Tatusev, R.L., Zhao, Q.,				
		Koonin, E.V. and Davis, R.W.				

TITLE	Genome sequence of an obligate intracellular pathogen of humans: <i>Chlamydia trachomatis</i>
JOURNAL	Science 282 (5389), 754-759 (1998)
MEDLINE	99000809
PUBMED	9784136
REFERENCE	2 (bases 1 to 14177)
AUTHORS	Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R. W., Olinger, L., Grimwood, J., Davis, R. W. and Stephens, R. S.
TITLE	Comparative genomes of <i>Chlamydia pneumoniae</i> and <i>C. trachomatis</i>
JOURNAL	Nat. Genet. 21 (4), 385-389 (1999)
MEDLINE	99206606
PUBMED	10192388
REFERENCE	3 (bases 1 to 14177)
AUTHORS	Stephens, R. S., Kalman, S., Lammel, C. J., Fan, J., Marathe, R., Atarvindh, L., Mitchell, W. P., Olinger, L., Tatuzov, R. L., Zhao, Q., Koonin, E. V. and Davis, R. W.
TITLE	Direct Submission
JOURNAL	Submitted (20-MAY-1998) Program in Infectious Diseases, University of California, 235 Warren Hall, Berkeley, CA 94720-7360, USA
FEATURES	Location/Qualifiers
SOURCE	1. 14177

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Oy 1861 gatcagaacacgacatcttcaagaacatcaagatccacaaagaagccatagattccat 1920
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Db 1647 CATTTCCAGTATCATGAGATTCTACCTCTTCAACCTCTGTGAATTAATCTCAATGAGGAA 1588
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RESULT 3
AX155940
LOCUS AX155940 2934 bp DNA
DEFINITION Sequence 183 from Patent WO0140474.
ACCESSION AX155940
VERSION AX155940.1 GI:14537039
KEYWORDS

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Oy	661	ggaaacggcaattcttlttgtagtaataactcgtactcttcttatacaataagccgt	720
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Oy	721	tgtgcaggaggaagcagatctcttcacctactgtcttccatacagaagaatcgtgttaac	780
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Oy	781	gtttccatacaacatcgcgtctttaaanaalgtagaacaagcttctcagaagcttcgat	840
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Oy	841	ggagaggaacttaagtaactactgcgctagatgttacaagcgaaatcgtgttagatctt	900
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Oy	901	tttagtaacaatatcacaaaaaalttggcgagcatttaagctctgtagttaccta	960
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Oy	961	gtggaataatggcccttacctacttataaacaatatgcgaataataaaggggcgctalc	1020
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Oy	1021	tatalagaaggaaccagcaactccaaaaattctgcgcgacgcgaigtatatlttlat	1080
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Oy	1261	ttcaataaggaagctgtatcaaaagagctcgtgtgtatlttcaaggagctacttcaatct	1320
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Oy	2403	agggaagcttcgtagtcaaaagatgggaagtgctgttttttttgcctccctatgaaacc	2462
Db	7685	AGCCTTCTTTAATTAACCCACACTTTGGTATCCCTCTGACAGTCGACATTTTACAGACTAG	7626
Oy	2463	cttggatcaagcatataactgacagctccctcttttagtgccttggtatattactcag	2522
Db	7625	AATACCCCGGACTCTGGAATGCCA---GCCCTTATCAAGTGCATTTGCTTGGCCTGTTC	7569
Oy	2523	ccgtgtcacttacttactgagtgaggagcctacccggaagcctttctacaagaactcctt	2582
Db	7568	CCAGGCGCTCGTTCCAGAAACATGGAACCCATATGAAGAAATTCATCCAAACATATCCCT	7509
Oy	2583	gataaagtctccatgctccctattgagttaaagtagacttaagaatgtctaccaagaacc	2642
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Oy	2823	tttccagatcatagatcttactactccttcctacacactctgttaattactcaatgvgggaat	2882
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RESULT	9				
LOCUS	AE002293				
DEFINITION	Chlamydia muridarum, section 25 of 85 of the complete genome.				
ACCESSION	AE002293	14482 bp	DNA	BCT	26-MAY-2000
VERSION	AE002293.1	GI:7190298			
KEYWORDS					
SOURCE	Chlamydia muridarum.				
ORGANISM	Chlamydia muridarum				
REFERENCE	Bacteria: Chlamydiales: Chlamydiaceae: Chlamydia.				
AUTHORS	1 (bases 1 to 14482)				
	Read, T.D., Hincham, R., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Berry, E.K., Peterson, J., Umayam, L.A., Ulteback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., Debroy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.				

McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.

Best Local Similarity	56.78;	Pred. NO.	0.95;
Matches	110;	Conservative	0;
Mismatches	81;	Indels	3;
Gaps			

SOURCE	ORGANISM
fruit fly.	<i>Drosophila melanogaster</i>

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VLMOOKLESPEFISFLDINSISSDGTATSHIKFSEDAFMAVYGSSESDNNKIRH
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FOLEKPIVDKFEADFDYITNIGSNLYFTNNDAPYRVIVDNNPAEHHTPIPE
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DIDIPMTIVORKDLAEPKGLYGGFNGSLMFMNDTDFGVAFPLR
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Matches 297; Conservative 0; Mismatches 658; Indels 1; Gaps 1;

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Db 220688 TTTAAATATATATTTTAAATTTTATGTCATTTTAAATACAGATTAACCTA 220629
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RESULT 13
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

Chlamydia muridarum.
Bacteria: Chlamydiales: Chlamydiaceae: Chlamydia.
1 (bases 1 to 12838)
Read,T.D., Brunham,R., Shen,C., Gill,S.R., Heidelberg,J.F.,
White,O., Hickey,E.K., Peterson,J.J., Unayam,L.A., Uettrback,T.,
Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
Genome sequences of Chlamydia trachomatis Mohn and Chlamydia
pneumoniae AR39

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
Nucleic Acids Res. 26 (6), 1397-1406 (2000)
10684935
2 (bases 1 to 12838)
Read,T.D., Brunham,R., Shen,C., Gill,S.R., Heidelberg,J.F.,
White,O., Hickey,E.K., Peterson,J.J., Unayam,L.A., Uettrback,T.,
Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA

RESULT	3	
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AC	AAA64753;	
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XX		
KW	Chlamydial infection; sexually transmitted disease;	
KW	pelvic inflammatory disease; PID; tubal obstruction; infertility;	
KW	trachoma; blindness; acute respiratory tract infection;	
KW	atherosclerosis; coronary heart disease; antibacterial; SS.	
XX		
OS	Chlamydia trachomatis.	
XX		
PN	WO200034483-A2.	
XX		
PD	15-JUN-2000.	
XX		
PF	08-DEC-1999;	99WO-US29012.
XX		
PR	08-DEC-1998;	98US-0208277.
PR	08-APR-1999;	99US-0288594.
PR	01-OCT-1999;	99US-0410568.
PR	22-OCT-1999;	99US-0426571.
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PI	Probst P, Bhattia A, Skeiky YAM, Fling SP, Jen S, Stromberg EJ;	
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DR	WPI; 2000-431303/37.	
XX		
PT	Isolated polypeptide for diagnosis and treatment of Chlamydia infection	
PT	comprises immunogenic portion of Chlamydia antigen, which comprises	
PT	amino acid sequence encoded by polynucleotide sequence -	
XX		
PS	Claim 1: Pages 173-174; 256pp; English.	

Query Match	97.38;	Score 2819.6;	DB 21;	Length 2895;
Best Local Similarity	98.68;	Pred. No. 0;		
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Oy	721	tgtgcagagagcgactcttctccctatactgcttctctaaaggaatgtgtataacat	780
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AC AAA64759:
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DT 02-FEB-2001 (first entry)
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KM Chlamydial infection; sexually transmitted disease;
KM pelvic inflammatory disease; PID; tubal obstruction; infertility;
KM trachoma; blindness; acute respiratory tract infection;
KM atherosclerosis; coronary heart disease; antibacterial; ss.
XX
OS Chlamydia trachomatis.
XX
PN MO20034483-A2.
XX
PD 15-JUN-2000.
XX
PF 08-DEC-1999: 99WO-US29012.
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PR 08-DEC-1998: 98US-0208277.
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PR 01-OCT-1999: 99US-0410568.
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XX
PA (CORI-) CORIXA CORP.
XX
PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Jen S, Stromberg EJ.
XX
DR WPI: 2000-431303/37.
XX
PT Isolated polypeptide for diagnosis and treatment of Chlamydia infection
PT comprises immunogenic portion of Chlamydia antigen, which comprises
PT amino acid sequence encoded by polynucleotide sequence
XX
PS Claim 1: Pages 200-201, 256pp: English.
XX
CC The present invention relates to new nucleic acid sequences and the
CC proteins encoded by the nucleic acid sequences. The encoded proteins
CC comprise an immunogenic portion of a Chlamydia antigen. The encoded
CC proteins are useful for the serodiagnosis and treatment of Chlamydia
CC infection. Chlamydiae are intracellular bacterial pathogens that are
CC responsible for a wide variety of human infections. C. trachomatis
CC infection is one of the most common sexually transmitted diseases and can
CC lead to pelvic inflammatory disease (PID), resulting in tubal obstruction
CC and infertility. Trachoma due to ocular infection with C. trachomatis is
CC the leading cause of preventable blindness worldwide. C. pneumonia is a
CC major cause of acute respiratory tract infections in humans and is also
CC thought to play a role in the pathogenesis of atherosclerosis and
CC coronary heart disease. The present sequence is a nucleic acid sequence
CC isolated in the present invention.
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SQ Sequence 2934 BP: 875 A; 645 C; 575 G; 839 T; 0 other:
Query Match 95.9%; Score 2777.8; DB 21; Length 2934;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2813; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
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Db 325 ttgcaaaaaatctacacccctgaagaagtggtgtgcatgtgttatagtcgatcccaatct 384
Oy 346 cctacccgtgagatctgtgatacaataagtgccctgtaacttttgataaaaaaactgtgtgc 405
Db 385 cctacccgtgagatctgtgatacaataagtgccctgtaacttttgataaaaaaactgtgtgc 444
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Db 445 agacacattacatcgagtaactcccaatgcaacttcaataaataagaagagcgagacc 501
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Db 502 attcatgctcaaaaatctttacataaataatcataatgaatgtgtgcggaatttatgaagac 561
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Db 562 ttctctatgtcgaaggagagccaatgtatccgctaataacctgtgtgtgagcgagaaat 621
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Db 1282 ggggtcctgtgtccttcaataaaggaagctgtatacaaacaggtcgtgtattttcagga 1341
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XX PS Claim 1; Page 207; 295pp; English.
CC The present nucleotide sequence is provided in a specification
CC relating to compounds and methods for the treatment and diagnosis of
CC chlamydial infection. The compounds provided include polypeptides and
CC fusion proteins comprising immunogenic portions of Chlamydia antigens
CC and DNA sequences encoding such polypeptides. They are useful for
CC vaccinating against chlamydial infection, which causes pelvic
CC inflammatory disease, trachoma, acute respiratory tract infections,
CC atherosclerosis and heart disease.
CC
CC
XX Sequence 2934 BP; 875 A; 645 C; 575 G; 839 T; 0 other:
SO
Query Match 95.9%; Score 2777.8; DB 22; Length 2934;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2813; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
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DB 85 ggactagctagaagaggtctctcttagaatcttcttatgcccgaactggtccagatcct 144
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DB 265 gctcgtgcacaataacagatgatacttaagctttttgtatcaccaaaagaaggttttat 324
QY 286 ttgtgaaaaaatctcacccctgaagaagtgtgtgctgattgtatgacggtcccaattct 345
DB 325 ttgtgaaaaaatctcacccctgaagaagtgtgtgctgattgtatgacggtcccaattct 384
QY 346 cctacgctggagatcgtgtatataaataaggtccgtcaatctttgaaataatactgtgtgc 405
DB 385 cctacgctggagatcgtgtatataaataaggtccgtcaatctttgaaataatactgtgtgc 444
QY 406 agacattatgaatcgaagaatcctaatatgacgtgtatataaataaggaagggcgagcc 465
DB 445 agacattatgaatcgaagaatcctaatatgacgtgtatataaataaggaagggcgagcc 501
QY 466 attcatgctcaaaatcttatataataataatcatatgatatgtgctggaattatgaagaac 525
DB 502 attcatgctcaaaatcttatataataataatcatatgatatgtgctggaattatgaagaac 561
QY 526 ttctctatgtcgaaggagagcattagtagccgctaataccttgtgttgagcgagaat 585
DB 562 ttctctatgtcgaaggagagcattagtagccgctaataccttgtgttgagcgagaat 621
QY 586 cagctctgttttcttttatgagacaactgttatccaactaatacagcagaagaaggt 645
DB 622 cagctctgttttcttttatgagacaactgttatccaactaatacagcagaagaaggt 681
QY 646 ggcgctatcctatgctggaagcagcaatcttttgagagtaaatctgcatctctctc 705
DB 682 ggcgctatcctatgctggaagcagcaatcttttgagagtaaatctgcatctctctc 741
QY 706 atcaataacgcctgtgtgcaaggagagcagatctctccctcatctgttctctaaagga 765
DB 742 atcaataacgcctgtgtgcaaggagagcagatctctccctcatctgttctctaaagga 801
QY 766 aatcgtgttaaatcgttttctatacaaatcgtctttaaanaatgtaaaacagcttct 825
DB 802 aatcgtgttaaatcgttttctatacaaatcgtctttaaanaatgtaaaacagcttct 861
QY 826 tcagaagcttctgataggaggaacatlaaagtaactcgcctgatatcttcagcgaat 885

DB 862 tcagaagcttctgataggaggaacatlaaagtaactcgcctgatatcttcagcgaat 921
QY 886 cgtgttagatcttttttagttacatatcacaaaaaatatggtcggaattttagct 945
DB 922 cgtgttagatcttttttagttacatatcacaaaaaatatggtcggaattttagct 981
QY 946 cctgttagttaccttagttgataatgcccctactactcttataaataatcgccaatat 1005
DB 982 cctgttagttaccttagttgataatgcccctactactcttataaataatcgccaatat 1041
QY 1006 aagggggagcctatcatatagaggaacacagcaactccaataattctgcgcagccgat 1065
DB 1042 aagggggagcctatcatatagaggaacacagcaactccaataattctgcgcagccgat 1101
QY 1066 gctattatttttaagaaatatgttgaataatgtaactgaatgtaacagtagc 1125
DB 1102 gctattatttttaagaaatatgttgaataatgtaactgaatgtaacagtagc 1161
QY 1126 tcagctaatcctccttagaagaataatgcaataacagtagcaagctctctgtgtaaatcta 1185
DB 1162 tcagctaatcctccttagaagaataatgcaataacagtagcaagctctctgtgtaaatcta 1221
QY 1186 ttagaagcaggagtagccaataatttaatttatgatcctatggaagttagcaatgca 1245
DB 1222 ttagaagcaggagtagccaataatttaatttatgatcctatggaagttagcaatgca 1281
QY 1246 ggggtctcgtgtctcttcaataaggaagtgtatcaaacggctctgtgtaatttcaaga 1305
DB 1282 ggggtctcgtgtctcttcaataaggaagtgtatcaaacggctctgtgtaatttcaaga 1341
QY 1306 gctactgttaattctgcgaattctcaacagcaatttcaacaaacaaacacctgcacc 1365
DB 1342 gctactgttaattctgcgaattctcaacagcaatttcaacaaacaaacacctgcacc 1401
QY 1366 ctactcctcgaataggtgtttctatgtatcgaagatcaltcgtcagcttaacgtatcga 1425
DB 1402 ctactcctcgaataggtgtttctatgtatcgaagatcaltcgtcagcttaacgtatcga 1461
QY 1426 ttcaacaaacgtgggggtgtgttctctcttggaattgagcaggtctgtgtgtcatataa 1485
DB 1462 ttcaacaaacgtgggggtgtgttctctcttggaattgagcaggtctgtgtgtcatataa 1521
QY 1486 aatgtgcaggaattctcgtacgaatgctcctataacacctaagaacatltgattgaat 1545
DB 1522 aatgtgcaggaattctcgtacgaatgctcctataacacctaagaacatltgattgaat 1581
QY 1546 cttcttccattctgaaaggtgtgtgctgagatctcttattgttgggtagagcctacaat 1605
DB 1582 cttcttccattctgaaaggtgtgtgctgagatctcttattgttgggtagagcctacaat 1641
QY 1606 aacagcaataactatacagcagatctgacgtactcctttcatltaagtatgtataaac 1665
DB 1642 aacagcaataactatacagcagatctgacgtactcctttcatltaagtatgtataaac 1701
QY 1666 tcaactatgtagctatgaggaattctccttataagatccaagatctaaacatgctgtg 1725
DB 1702 tcaactatgtagctatgaggaattctccttataagatccaagatctaaacatgctgtg 1761
QY 1726 tcatcagacgtatgctatctatcttctgaggtcagtgatgataaacgcgtaaagatcgtatg 1785
DB 1762 tcatcagacgtatgctatctatcttctgaggtcagtgatgataaacgcgtaaagatcgtatg 1821
QY 1786 atggaatttttgggactaaatgctcctcatltaagtatgtagcagagacttggagcttggggc 1845
DB 1822 atggaatttttgggactaaatgctcctcatltaagtatgtagcagagacttggagcttggggc 1881
QY 1846 tgggcaaaacccaagatccagaacagcatctcagcaacatccagatccacaanaa 1905
DB 1882 tgggcaaaacccaagatccagaacagcatctcagcaacatccagatccacaanaa 1941
QY 1906 gccaatagatccatagaaacttatctagcttggctcctgctgtggatgtatcccttagc 1965
DB 1942 gccaatagatccatagaaacttatctagcttggctcctgctgtggatgtatcccttagc 2001

PR 02-NOV-1998; 98US-0107035.

PA (CONN-) CONNAUGHT LAB LTD.

PI Murdin AD, Oomen RP, Wang J;

DR WPI; 2000-350688/30

DR P-PSDB; AAY92832.

PT Chlamydia antigens and the proteins they encode, useful for
PT vaccinating against Chlamydia infections that affect the respiratory
PT tract

PS Claim 2; Fig 21; 226pp; English

The nucleic acids may be used for the recombinant production of the *Chlamydia* polypeptides (either *in vivo* or *in vitro*) according to standard recombinant DNA methodologies. The polypeptides may then be used to vaccinate against *Chlamydia* infections in mammals. *Chlamydia*, such as *C. pneumoniae*, are pathogens responsible for upper respiratory tract infections such as community acquired pneumonia, acute respiratory disease and bronchitis and may be implicated in atherosclerotic changes and asthma. The nucleic acids may also be used as probes for detecting the presence of *Chlamydia* nucleic acids in samples, and therefore (diagnose infections) and the proteins may be used as antigens for the production of antibodies that may be used to detect *Chlamydia* proteins in samples (e.g. via enzyme linked immunosorbent assay (ELISA)).

50 Sequence 3003 BP; 868 A; 741 C; 563 G; 831 T; 0 other;

Query Match	4.5%	Score 131.6;	DB 21;	Length 3003;
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Matches 759; Conservative 0; Mismatches 859; Indels 42; Gaps 7;

QY	1253	ctgtgctctcaataaagaagcgcgtacaaacagccctgttagtttttcaggagtaactg	13112
Db	1370	ctcttaatctttaaaccccaatgcaaccacacacaggaacgacttattttcttcagccta	14299
QY	1313	ttaattctgcagatttttcatlcaacgcgaatttlaacaaacaaacacctgcaccccttact	13722
Db	1430	tcccagaagcttctgacttaccgaataatttcaatttagcagctcggaataatactctgac	14899
QY	1373	tcagtaatggttttctctatgtatctgaagaacatgctcaacttcagtctatgattcaaac	14222
Db	1490	tctgcgaatggtctctctctcatcgaagatctgctggaatcgcgaatctataagttcaatc	15499
QY	1433	aaactggggggtgtgtttctctcttgggaatggagcagttctggatgtgtcataaattgtg	14922
Db	1550	aaaaagagagatcctctaatttgagcagcgcgagctattgcaacaactgcgaactctg	16099
QY	1493	caggaaatctcgtcagcaatgctctataaacctgaaacatatgtgattgaaacttctct	15522
Db	1610	agactccatacaactagttagctccacagtlcatlcatlaactgtgattaaacctcc	16699
QY	1553	ccattctcgaaaagcggcgcgagatctccttatctgtgggtagaagctcaacaaataacagca	16122
Db	1670	ccctgactcttgcaaaaaggaagagctcctcaactcttgtagctccgctcccttacaactagt	17299
QY	1613	ataactatcacgcagatacgcgcagctcaacttttcatlaagtatglaaanaactcaca	16722
Db	1730	ctccttccacagaggaacataaacctcaattacttaccagtctcctcgaacacct	17866
QY	1673	tgtatgactatrggaattctcctctatgaaatccacagatccaaacccaatgctctgtcataac	17222
Db	1787	ttaaagtgaagaaacccgagatccctacacaglaataagatctctgagccatttacaanaa	18466
QY	1733	agccatgctatctatctcttgagcgtatgataacagcctlaagatctgtatgtatgagtt	17922
Db	1847	ttaactcttcttcttatacggatgtaacagcacgcatatcatatcacatacgtatacttcatc	19066
QY	1793	tttcggagcaaatgtctcctcctcattatgatacgaagactttgagattgggcttgcg	18499

Dh	1907	ctgaagcttaaatgctgcagcagcattacggttatagaagctctgcgtctcctattgg	1966
Oy	1850	caaaaaactcaagctccgaagaccgacatctctcagccaacatccagatccacaaaagcca	1909
Dh	1967	-----tagagacgataacaacaacaataagctctctctatagagcgcga	2011
Oy	1910	atagatccatagaaccttcttaactgaacttgctctccctcctcgtgfatgttcttagccga	1965
Dh	2012	aacaccctcaagagctctctttagccaatgtagctccctcttagatataagytcaatccgt	2071
Oy	1970	aacgaggaagccccctcatagcggaataaccttagg-----ggagatagctgctgca	2023
Dh	2072	aatcccaaggagatctctgctacgactccctcccttagagcaatcccttcatatagtctctc	2131
Oy	2024	cagaagaacttaaaaaatagtcgcgaactgacacactglatcatccctctcttctgaggaata	2083
Dh	2132	tatttaagaagtataatactgaactcgtgattctgatatatcgagggccctctcttagaact	2191
Oy	2084	caggaagaaggaactagcgcatgattggtttaccagaatccctcgagaaaatactcttgattcc	2143
Dh	2192	aaggaatgctcggaagggccctcttgcttcatataaaatagcattcccggggtctccagattcc	2251
Oy	2144	ataagcctctctccggatctc-----tgcgggagtgtatgacgagcgacacacact	2197
Dh	2252	gtatcccaatctaacggggtattctcttaacaaacatccctcggaaactccttatactagaata	2311
Oy	2198	tctatctgaatctagatcgaactgaacccaacaaactcaatagaggtttagcgcaaaaaaacag	2257
Dh	2312	ctcctcttaggtttgacacagttctcttaecccgccgactaagaataatcgatccaagcaacag	2371
Oy	2258	tatctcttaaaaattactcatgccaagagagaatgctctctctcatatgcaagaagttctc	2317
Dh	2372	ctctgcgctcaacaatcacagctctctctcaatttatgttagcttcgggtgtccaaagagct	2431
Oy	2318	tgctgcactaaattatgtggcgctttaaagcgatgagacataactgctccaatttctata	2377
Dh	2432	ctgcaacatcccaaggtttagcglatggtctatggttggagccataac---ctccagcctba	2488
Oy	2378	ccaagaaggaanaactcaacatctcaacgagagcggttccgtagtcaaacgagtggaggtgtg	2437
Dh	2489	tcgctcaacataagaacaagggcgaagagcggtgtatatgcatacatatagagaagcta	2548
Oy	2438	tttttttgatctccctaagaaacctttgatacgaacgatatgaactgacagctcccttt	2497
Dh	2549	tcggctgtctctctcccttgccaac-----agaaatccatacttcaacctcaagccggtctg	2602
Oy	2448	tagtgtctcttgatattatctcttagcctgctctcaacttaactgagggggagctctccgcg	2557
Dh	2603	ctcaggaatgccaatcgatcgttcttccaacaaaacagcggttcgaagaagtctgtagcaatccc	2662
Oy	2558	gaagctcttcttacaagaagacctcttgcataatgtccctagctccatagtgagttaaagta	2617
Dh	2663	gaaagtgtgtctctccaaaagcctttctcatabatctgtgaccttaaccttaggaatccaagaa	2722
Oy	2618	gcttatagaatgctacccaagaagacctcaagcctggaactgtagaattggtacatccaacccg	2677
Dh	2723	aatggcagctcaaaatctccacgttaacctacagaatgagctctagaacttcttcaacaacgg	2782
Oy	2678	cttcgtataagcaagaaccgagatcgcgacccagctctcttagcgcaagtaagggtatttgt	2733
Dh	2783	tacttataccaacaaaatcccnaaatcggtgtcagcctactcttgagcggaaggtctccggg	2842
Oy	2738	cttgtagtggagagccctctacgtgctgatacgatgctccataaaactcacagccaacac	2797
Dh	2843	ataccctagccaataactaagtttcgcgaatgctttaggtgtacaagaagtccaatacaactg	2907
Oy	2798	aaccttttaggttttaactctccatcttcagatataagatgatactcctctcaacct	2857
Dh	2903	cgctcttcggtctctcgtatcatctctttagattacaagaagtgcgtctcctctcgat	2962
Oy	2858	ctctgtaattcatctaatggtggaaatgctctcgatctca	2897
Dh	2963	ctacgcaccactctccaagcaggaaagtacctaataattca	3002

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Db 2532 ttgcaacatcccaagcttagctgctatggtggtggtacacac---ctccagcctaca 2588
Qy 2378 cccaagagaaataatcaatctcaaggagcttccgtgttcaaaagatggagtgctg 2437
Db 2589 tccgtcacatcaagaacagagagagacgtgtatagccatacatatagacagagcta 2648
Qy 2438 tttttttgacccctcaagaaccccttggatcaacgatatagcagacgtcccttt 2497
Db 2649 tggcctgttcttcccttggcaac-----agaaatccatcttccacccagccgttgc 2702
Qy 2498 taggtgtctgtgtatattatctagcctgtctcaacttactagtgaggagccatccgc 2557
Db 2703 ttcaggaattgtcaatagcttctcaccacaacagcgttcgaagatgtgtgacaatcccc 2762
Qy 2558 gaagctttctcaagaagactcctttgatcaatgctcctatgcttatgtgataagcta 2617
Db 2763 gaaggtttgtcttcaaaagccttctatatacttgacacttcaagcttagaattccaagaa 2822
Qy 2618 gcttatatgactgtacccaagaacctcaagcctgagctgtagaattggtacataccaacgcg 2677
Db 2823 aatgtgagtgcaaatctccagtaacctacagatgtagaacttttaccacaacgcg 2882
Qy 2678 ttctgtatagaagaacacagagatcgacccagctccttagcagtaagggtatttgg 2737
Db 2883 tactatcaacaacaaatcccccaatcggtgtcagctacttgcgagcgaggttccctgg 2942
Qy 2738 ttgtgtatgtgaagccctcatcgctcatgcatgtcctataaatactcaagcaaac 2797
Db 2943 atatccaaagacataactatgttgcgaatgttlaaggatcaaaagccacaatcaaacctg 3002
Qy 2798 aacctgtgtgtgttaacttccatccatgcatgattctcctccttcaacct 2857
Db 3003 cgcctctcgttctcctcgtctcatcttcttgataccagaagatcggtcctcctcgtgaat 3062
Qy 2858 tctgtaatactcaatggggaatgtctctgcgattcta 2897
Db 3063 ctacgcacatctccaagcagagagtaacttaaatctta 3102

RESULT 10
AAFS8252/C
ID AAF58252 standard: DNA: 936 BP.
XX
AC AAF58252:
XX
XX 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1835.
XX
KM Electron-transfer group: ETM; mismatch: genotyping;
XX
KW gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000: 2000WO-US20476.
XX
PR 26-JUL-1999: 99US-0145695.
XX
PR 17-MAR-2000: 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM:
XX
XX WPI: 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
XX PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX PT a single surface

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XX
PS Example 6: Page 127; 1599P; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other:

Query Match 4.1%; Score 118.6; DB 22; Length 936;
Best Local Similarity 1.3%; Pred. No. 2,8e-23;
Matches 10; Conservative 480; Mismatches 299; Indels 0; Gaps 0;

Qy 436 gctgttaataaataagagaagcgagacatcatcgtcctcaaatcttaacataatcat 495
Db 789 GCGWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 730
Qy 496 aatcatgactgtgtcgtatattgaagaactttctatgtccgaggagagccattagt 555
Db 729 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 670
Qy 556 accgctaactctgtgtgagcgagaatcagctctgttctcttattgagacaacatc 615
Db 669 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 610
Qy 616 tgtatcaactaatacagcaggaagaagtgcgctatctatgtcgtgaaagcaattct 675
Db 609 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 550
Qy 676 ttggaagataaactcgcgtatctcttctatcaataagcctgtgtgcagagagagcg 735
Db 549 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 490
Qy 736 atcttccctcatctgttctcctcaaggaatcgtgtgaacatcgtttctataacat 795
Db 489 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 430
Qy 796 cgcgtttaaataatgtagaacaagcttctcagaagcttctgtagagagcaattaa 855
Db 429 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 370
Qy 856 gtaactactcgcctagaatgttaacagcaatcgtgtgtagagatctttttgtgacaatc 915
Db 369 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 310
Qy 916 acaaaaatattgvcgagctattagcctcctgttagtaccctagtgataatgcct 975
Db 309 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 250
Qy 976 acctacttataaacaatacgcgaataaagaaggcgctatctatataagaggaacc 1035
Db 249 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 190
Qy 1036 agcaactccaataatctcgcgcgacgcgcacatgcataattttaataaataatgtgact 1095
Db 189 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 130
Qy 1096 aatgtaactaatgcaatgttacccagtagctgaagctaatccctcctagaagaatgcat 1155
Db 129 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 70
Qy 1156 acagtagaagctcctcgtgtaattctatagagcagagtagccaaaattaat 1215
Db 69 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 10
Qy 1216 tttaatgat 1224
Db 9 WWWWWWWWWWW 1

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CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.

Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

Query Match 4.1%; Score 118.6; DB 22; Length 936;
Best Local Similarity 1.3%; Pred. No. 2.8e-23;
Matches 10; Conservative 480; Mismatches 299; Indels 0; Gaps 0;

```
Qy 436 gctgttaataaagaagcgagcattcttcctcaaatcttacaatacat 495
Db 789 GCMWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 730
Qy 496 aatcatgatggtcggaatttaagaactttctatgctcgaggaagcattagt 555
Db 729 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 670
Qy 556 accgctaacttctgtgtgagcgagatcgtctgttctctttatgacaacatc 615
Db 669 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 610
Qy 616 tgtattcaactaatacagcaggaaggtgctgctatctatgctggaagcattct 675
Db 609 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 550
Qy 676 ttgagagaataactgcatctctcttatacaaacgctgtgtgcaagagagcg 735
Db 549 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 490
Qy 736 atctctccctatactgttctcttaacagaaatcgtgtgaacatgctttcatacaat 795
Db 489 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 430
Qy 796 cgtgctttaaaaagttagaagaagcttctcaagaagcttcgtagagagaaatlaa 855
Db 429 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 370
Qy 856 gtaactactgcctagaatgttaacagcaatcgtgtgagagatcttttagtgacaatc 915
Db 369 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 310
Qy 916 acaaaaataatggtcgagctattacgctcgtgtgtaacctagtgataatgacct 975
Db 309 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 250
Qy 976 acctacttataaacaatcgcacaataaagggcgctatctatataagacgaac 1035
Db 249 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 190
Qy 1036 agcaactccaatctctgcgacgcacgtctatattttaagaataatgtgact 1095
Db 189 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 130
Qy 1096 aatgtaactaagcaaatggtacagtaacgtcaatccctcctgaagaatgcaata 1155
Db 129 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 70
Qy 1156 acgtatgaagcctcctgtgtaaatctatagagcagggagtagcacaattaat 1215
Db 69 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 10
Qy 1216 tttaatgat 1224
Db 9 WWWWWWWWWWW 1
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RESULT 13
AAFS8259/c
ID AAF58259 standard; DNA: 936 BP.
XX

```
AC AAF58259;
XX 24-APR-2001 (first entry)
DT 24-APR-2001 (first entry)
XX 24-APR-2001 (first entry)
DE Oligonucleotide D2004.
XX Oligonucleotide D2004.
KW Election-transfer group: ETM; mismatch; genotyping;
XX gene expression; ss.
OS Synthetic.
XX WO200107665-A2.
XX 01-FEB-2001.
XX 26-JUL-2000; 2000WO-US20476.
XX 26-JUL-1999; 99US-0145695.
XX 17-MAR-2000; 2000US-0190259.
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX UmeX RM.
XX WPI: 2001-159728/16.
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface.
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XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
XX
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Query Match 4.1%; Score 118.6; DB 22; Length 936;
Best Local Similarity 1.3%; Pred. No. 2.8e-23;
Matches 10; Conservative 480; Mismatches 299; Indels 0; Gaps 0;

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Qy 436 gctgttaataaagaagcgagcattcttcctcaaatcttacaatacat 495
Db 789 GCMWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 730
Qy 496 aatcatgatggtcggaatttaagaactttctatgctcgaggaagcattagt 555
Db 729 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 670
Qy 556 accgctaacttctgtgtgagcgagatcgtctgttctcttatagacaacatc 615
Db 669 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 610
Qy 616 tgtattcaactaatacagcaggaaggtgctgctatctatgctggaagcaattct 675
Db 609 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 550
Qy 676 ttgagagaataactgcatctctcttatacaaacgctgtgtgcaagagagcg 735
Db 549 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 490
Qy 736 atctctccctatactgttctcttaacagaaatcgtgtgatacgtttcatacaat 795
Db 489 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 430
Qy 796 cgtgctttaaaaagttagaagaagcttctcaagaagcttcgtagagagaaatlaa 855
Db 429 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 370
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 05:09:28 ; Search time 59.26 Seconds
(without alignments)
11075.485 Million cell updates/sec

Title: US-09-677-752-1
Perfect score: 2898
Sequence: 1 aagaaagcgcttcttctt.....aaatgtctgcgattctag 2898

Scoring table:
IDENTITY_NMC
Gapop 10.0 , Gapext 1.0

Searched: 351203 segs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCtUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Backfilest1.seq:*

* Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	40.6	1.4	1122	2	US-08-915-107-3 Sequence 3, Appli
C 2	40.6	1.4	1122	4	US-09-273-613-3 Sequence 3, Appli
C 3	40.6	1.4	1125	4	US-08-915-107-1 Sequence 1, Appli
C 4	40.6	1.4	1125	4	US-09-273-613-1 Sequence 1, Appli
5	39.2	1.4	1560	1	US-08-356-180-1 Sequence 1, Appli
6	38.4	1.3	807	3	US-08-718-905-1 Sequence 1, Appli
7	38.4	1.3	807	4	US-09-550-497-1 Sequence 1, Appli
8	36.2	1.2	1311	4	US-08-584-760A-66 Sequence 66, Appli
9	35.4	1.2	3513	1	US-07-828-788A-5 Sequence 5, Appli
10	35.4	1.2	3513	1	US-08-278-685-1 Sequence 1, Appli
11	35.4	1.2	3513	1	US-08-278-685-3 Sequence 3, Appli
12	35.4	1.2	3513	1	US-08-277-721-1 Sequence 1, Appli
13	35.4	1.2	3513	1	US-08-277-721-3 Sequence 3, Appli
14	35.4	1.2	3513	1	US-08-602-737-3 Sequence 3, Appli
15	35.4	1.2	3513	4	US-09-001-982-3 Sequence 3, Appli
16	35.4	1.2	3513	5	PCt-US92-11337-5 Sequence 5, Appli
17	35	1.2	6909	2	US-08-804-196-1 Sequence 1, Appli
18	35	1.2	6909	2	US-08-658-340-1 Sequence 1, Appli
19	35	1.2	6909	3	US-08-746-111-26 Sequence 26, Appli
C 20	34.6	1.2	1901	4	US-09-338-907-181 Sequence 181, App
C 21	34.6	1.2	56516	2	US-08-996-306-1 Sequence 1, Appli
C 22	34.6	1.2	56516	4	US-09-338-907-1 Sequence 1, Appli
C 23	34.6	1.2	56520	4	US-09-338-907-179 Sequence 179, App
C 24	34	1.2	486	4	US-09-328-111-363 Sequence 363, App
C 25	34	1.2	2689	1	US-08-465-795-2 Sequence 2, Appli
C 26	34	1.2	5589	1	US-08-465-795-1 Sequence 1, Appli
C 27	33.8	1.2	740	4	US-09-451-117-1 Sequence 1, Appli

28	33.4	1.2	8920	2	US-08-446-855A-1 Sequence 1, Appli
29	33.4	1.2	8920	4	US-09-150-741-1 Sequence 1, Appli
30	33.2	1.1	414	2	US-08-630-822A-63 Sequence 63, Appli
31	33.2	1.1	414	2	US-09-005-069-63 Sequence 63, Appli
32	33.2	1.1	2848	3	US-08-539-205A-3 Sequence 3, Appli
33	33.2	1.1	19124	2	US-07-487-826B-13 Sequence 32, Appli
34	33	1.1	660	1	US-07-991-867B-32 Sequence 32, Appli
35	33	1.1	660	2	US-08-107-755A-32 Sequence 32, Appli
36	33	1.1	660	2	US-08-544-332-32 Sequence 32, Appli
37	33	1.1	1511	1	US-07-991-867B-8 Sequence 8, Appli
38	33	1.1	1511	1	US-08-107-755A-8 Sequence 8, Appli
39	33	1.1	1511	2	US-08-544-332-8 Sequence 8, Appli
40	33	1.1	4810	3	US-08-852-629-11 Sequence 11, Appli
41	33	1.1	4838	3	US-08-852-629-15 Sequence 15, Appli
42	33	1.1	5658	4	US-08-881-450A-23 Sequence 23, Appli
43	32.6	1.1	2287	4	US-08-845-258-8 Sequence 8, Appli
44	32.6	1.1	2287	4	US-08-990-571-8 Sequence 8, Appli
45	32.6	1.1	2287	4	US-08-723-142A-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-915-107-3/c
: Sequence 3, Application US/08915107
: Patent No. 5885805
: GENERAL INFORMATION:
: APPLICANT: Burnham, Martin K.R.
: APPLICANT: Lonetto, Michael A.
: APPLICANT: Warren, Patrick V.
: TITLE OF INVENTION: NOVEL Gbpa
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESS: Dechert Price & Rhoads
: STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
: CITY: Philadelphia
: STATE: PA
: COUNTRY: US
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/915.107
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Dickinson, Todd O
: REGISTRATION NUMBER: 28, 354
: REFERENCE/DOCKET NUMBER: P50549-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-994-2252
: TELEFAX: 215-994-2222
: TELEX:
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1122 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: US-08-915-107-3
: Query Match 1.4%; Score 40.6; DB 2; Length 1122;
: Best Local Similarity 46.3%; Pred. No. 0.040;
: Matches 133; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

OY 1520 taacacitgaagcatattgagatgaatcttcttcacattctgaagaagtgtgctgagattc 1579
DB 883 TAAATATGTTGATATCTTAATTAATTCATAAGTTGTTCTTAATTAATGCAATCTAATCTCG 824
OY 1580 cttatttgggttagagcctacaataacagacaataacatacagagaactgagctta 1639
DB 823 GTTCTTCGATACCTTAATATCTTTAAGACATTTCTTTATCTTCATCATCTAATGTAAGCA 764
OY 1640 cctttcattaaagtgtgtaaaacttcacatcattgattgactaaggaattctcctatg 1699
DB 763 TTCTCTTTCATTTTTCGACTAATTAACAATCATTGACAGTCTCTGCGTGCATATT 704
OY 1700 aatccacagatctaacccatgctgctgctacacagcctatgctatct 1746
DB 703 CACGAATCGCTTTACTTTATCATTAATCATCATCACCAATTTCACTCT 657

RESULT 4

US-09-273-613-1/C
Sequence 1, Application US/09273613
Patent No. 6203800
GENERAL INFORMATION:
APPLICANT: Burnham, Martin K.R.
APPLICANT: Lonetto, Michael A.
APPLICANT: Warren, Patrick V.
TITLE OF INVENTION: NOVEL Gbpa
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/915,107
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50549-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-273-613-1

Query Match 1.4%: Score 40.6; DB 4; Length 1125;
Best Local Similarity 46.3%; Pred. No. 0.048;
Matches 133; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

OY 1460 atgagacagttctgtgattgataaataatggtgcaggaattctgtgtagcaatgctctta 1519
DB 943 ATTGAGGTGCGAGTACATACCTGTTTAATGTCCAAGCAGTACTTCTTGACACACGACG 884
OY 1520 taacacitgaagcatattgagatgaatcttcttcacattctgaagaagtgtgctgagattc 1579

DB 883 TAAATATGTTGATATCTTAATTAATTCATAAGTTGTTCTTAATTAATGCAATCTAATCTCG 824
OY 1580 cttatttgggttagagcctacaataacagacaataacatacagagaactgagctta 1639
DB 823 GTTCTTCGATACCTTAATATCTTTAAGACATTTCTTTATCTTCATCATCTAATGTAAGCA 764
OY 1640 cctttcattaaagtgtgtaaaacttcacatcattgattgactaaggaattctcctatg 1699
DB 763 TTCTCTTTCATTTTTCGACTAATTAACAATCATTGACAGTCTCTGCGTGCATATT 704
OY 1700 aatccacagatctaacccatgctgctgctacacagcctatgctatct 1746
DB 703 CACGAATCGCTTTACTTTATCATTAATCATCATCACCAATTTCACTCT 657

RESULT 5

US-08-356-180-1
Sequence 1, Application US/08356180
Patent No. 5762924
GENERAL INFORMATION:
APPLICANT: DALL, DAVID J.
APPLICANT: FERNON, CAROL A.
APPLICANT: SRISKANTHA, ALAGACONE
TITLE OF INVENTION: RECOMBINANT ENTOMOPOXVIRUS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC AND BECKER
STREET: 99 CANAL CENTER PLAZA, SUITE 300
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,180
FILING DATE: 16-DEC-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MILLS, DEMETRA J.
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 1451-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
TELEX: AMERPAT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-356-180-1

Query Match 1.4%: Score 39.2; DB 1; Length 1560;
Best Local Similarity 48.6%; Pred. No. 0.14;
Matches 107; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

OY 783 ttctataacaatgcgtgctttaaanaatgtagaacaagcttctcagaagcttctgtag 842
DB 748 TTTCACACAAATGTAGTACTTACCAATTTATGCCGCCGCGAGCCGATGTTGGAGT 807
OY 843 aggaagcaattaaagtaactactgctgcttagatggttacaagcaatcggtgtagatctttt 902
DB 808 AGTTCATTGCGAGTATAGAGATGAGATGATTTTGGCAGGAATTTGGTACTACCTTAT 867
OY 903 tagtagacataatcacaanaaattatggtgcgagctattatgagctctcctgtagttaccctagt 962

[illegible]

CLONE: 81F

? ORGANISM: BACILLUS THURINGIENSIS
 ? STRAIN: KENYAE
 ? INDIVIDUAL ISOLATE: PS81F
 ? IMMEDIATE SOURCE:
 ? LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
 ? CLONE: 81F
 ? US-07-828-788A-5

sequence of applications 00/00277722

STATE: California
COUNTRY: USA

COUNTRY: USA

Wed Apr 24 09:33:43 2002

us-09-677-752-1.rml

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 05:12:13 ; Search time 40.76 Seconds
(without alignments)
10652.069 Million cell updates/sec

Title: US-09-677-752-1

Perfect score: 2898
Sequence: 1 atgaaaaaaggttttctt.....aattgtctgcgattctag 2898

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 12861 seqs, 7490995 residues

Total number of hits satisfying chosen parameters: 257722

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	48.4	1.7	1511	US-09-612-402A-10	Sequence 10, Appl
2	48.4	1.7	1515	US-09-612-402A-22	Sequence 22, Appl
3	48.4	1.7	4435	US-09-612-402A-1	Sequence 1, Appl
4	45.2	1.6	3324	US-09-612-402A-24	Sequence 24, Appl
5	42	1.4	3354	US-09-612-402A-23	Sequence 23, Appl
6	40.8	1.4	5621	US-09-630-630B-23	Sequence 23, Appl
7	40	1.4	3996	PCT-US02-06415-42	Sequence 42, Appl
8	38.2	1.3	9477	US-10-105-299-13241	Sequence 13241, A
9	38.2	1.3	9466	US-10-105-299-13242	Sequence 13242, A
10	37.4	1.3	282	US-09-789-189-553	Sequence 553, Appl
11	36.6	1.3	912	US-09-828-523A-19	Sequence 19, Appl
12	36.6	1.3	936	US-09-828-523A-85	Sequence 85, Appl
13	36.4	1.3	277	US-09-540-210B-15021	Sequence 15021, A
14	35.4	1.2	4205	US-10-105-299-13644	Sequence 13644, A
15	35.2	1.2	1481	US-10-105-299-2465	Sequence 2465, Ap
16	34.6	1.2	682	US-10-089-128-31	Sequence 31, Appl
17	34.2	1.2	4017	US-09-648-692B-10	Sequence 10, Appl
18	33.6	1.2	498	US-10-099-926-1619	Sequence 1619, Ap
19	33.2	1.1	12604	US-10-105-299-6697	Sequence 6697, Ap
20	33.2	1.1	298	US-09-685-209A-475	Sequence 475, Ap
21	33	1.1	2791	US-10-105-299-1300	Sequence 1300, Ap
22	33	1.1	2791	US-10-105-299-1301	Sequence 1301, Ap
23	33	1.1	2791	US-10-106-698-1534	Sequence 1534, Ap
24	32.8	1.1	16285	US-10-105-299-9034	Sequence 9034, Ap
25	32.8	1.1	16285	US-10-105-299-9035	Sequence 9035, Ap
26	32.4	1.1	789	US-09-540-209B-361	Sequence 361, Appl

C 27	32.4	1.1	17646	US-10-105-299-6422	Sequence 6422, Ap
C 28	32.4	1.1	17646	US-10-105-299-6424	Sequence 6424, Ap
C 29	32.2	1.1	294	US-09-540-210B-13065	Sequence 13065, A
C 30	32.2	1.1	6483	US-10-105-299-12426	Sequence 12426, A
C 31	32.2	1.1	6483	US-10-105-299-12427	Sequence 12427, A
C 32	32	1.1	6844	US-10-105-299-10429	Sequence 10429, A
C 33	32	1.1	6937	US-10-105-299-11722	Sequence 11722, A
C 34	32	1.1	13608	US-10-105-299-9203	Sequence 9203, Ap
C 35	32	1.1	12073	US-10-105-299-7267	Sequence 7267, Ap
C 36	32	1.1	22073	US-10-105-299-9014	Sequence 9014, Ap
C 37	32	1.1	22958	US-10-105-299-11723	Sequence 11723, A
C 38	32	1.1	40898	US-10-105-299-12480	Sequence 12480, A
C 39	31.8	1.1	231	US-09-540-210B-26664	Sequence 26664, A
C 40	31.8	1.1	11343	US-10-105-299-9409	Sequence 9409, Ap
C 41	31.8	1.1	11343	US-10-105-299-9411	Sequence 9411, Ap
C 42	31.6	1.1	474	US-10-097-105-435	Sequence 435, Ap
C 43	31.6	1.1	733	US-10-106-698-472	Sequence 472, Ap
C 44	31.6	1.1	2277	US-10-105-299-8237	Sequence 8237, Ap
C 45	31.6	1.1	2277	US-10-105-299-8238	Sequence 8238, Ap

ALIGNMENTS

RESULT 1
US-09-612-402A-10
Sequence 10, Application US/09612402A
GENERAL INFORMATION:
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
FILE REFERENCE: 7969-086-999
CURRENT APPLICATION NUMBER: US/09/612,402A
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 08/942,596
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ IDS NOS: 43
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 1511
TYPE: DNA
ORGANISM: Chlamydia sp.
US-09-612-402A-10

Query Match 1.7% Score 48.4 DB 5 Length 1511
Best Local Similarity 56.7% Pred. No. 0.0092
Matches 110; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

OY 896 tcttttagtgcataatcacaataattatgcgcgagctattagcttctgtagta 955
Db 1007 tttcttagtagaagatcgtcgtcggaaggagcattatgcacaaagctc 1066
OY 956 ccctagtgagataagcgcctcctacttataacaatattcgcgcgaccgcaatgctat 1015
Db 1067 cgttgcctactcgtgcgcctcctacttataacaatattcgcgcgaccgcaatgctat 1123
OY 1016 ctactatataagcgaacccagcaatcccaaatattcgcgcgaccgcaatgctat 1075
Db 1124 cgatttcttagtagaagatcgtcgtcggaagcgttattcgtcgtatgagagatatatt 1183
OY 1076 ttaatgaataatt 1089
Db 1184 ttagatgggaatcct 1197

RESULT 2
US-09-612-402A-22
Sequence 22, Application US/09612402A
GENERAL INFORMATION:
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof

Query Match	1.4%	Score 40.8	DB 5	Length 5621
Best Local Similarity	44.7%	Pred. No. 0.88		
Matches	159	Conservative	0	Mismatches 197
				Indels 0
				Gaps 0
Qy 1223	atccattgaagttagcaaatgcaaggggtctctgtgtccttcataaagaagctgatalcaaa			1282
Db 1666	atcgaaagacaagatagaagaagccgtagccgtgagcgaatcactgttaattatgtgtcaa			1725
Qy 1283	caggctctgtagtatttcagagagctacgtgtaattctgcagatttcataatccaagcaatt			1342
Db 1726	acttaatcgaaacagcttggcgcaactcgtatgattgtcggttagaactaacatgcaccacaa			1785
Qy 1343	tacacaacaaaacacctgacacccctactctcaagtaatggtttctcatgatalogaatgc			1402
Db 1786	tccaagattcttctgtatcttcattccaattgacacacttaatggtgtgccaattctgtctaaac			1845
Qy 1403	atgctcagcttacagaggaatgcattacacaaactcgtgggtgtgtttttttctcttggaatg			1462
Db 1846	attcaagaatgatccgaattataaccacgaagaatgtgtcgtgtgtttacacagaccatg			1905

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RESULT      8
US-10-105-299-13241/c
: Sequence 13241: Application US/10105299
:
: GENERAL INFORMATION:
:
: APPLICANT: Rosen, et. al
:
: TITLE OF INVENTION: Human Secreted Proteins
:
: FILE REFERENCE: P5950
:
: CURRENT APPLICATION NUMBER: US/10/105,299
:
: CURRENT FILING DATE: 2002-03-26
:
: NUMBER OF SEQ. ID NOS: 15197
:
: Prior Application removed - See File Wrapper or Palm
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 13241
:
: LENGTH: 9477
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
US-10-105-299-13241

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Query Match 1.3%: Score 36.6; DB 5; Length 936;
Best Local Similarity 51.5%: Pred. No. 5.6;
Matches 84; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 330 tgcgaatcccaattctccaccgtgagatcgtgtatcaatgagcccttaacttga 389
Db 201 tgcgaatcccaattctccaccgtgagatcgtgtatcaatgagcccttaacttga 142
Qy 390 aataaactgttcgacacattacatcgagtaacatgcagcgttaataaat 449
Db 141 CATACACACGTGTGATATCTACACAAATATCCATGCTCTTAACATTGAAT 82
Qy 450 aagagaagcgagccattcatctcaaatcttaataat 492
Db 81 AACCAAGATTACTGCGCCAGATAAACCCTTACAACTAAT 39

RESULT 13
US-09-540-210B-15021/C

Sequence 15021, Application US/09540210B

GENERAL INFORMATION:
APPLICANT: Sellhammer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: PD-1037 CIP
CURRENT APPLICATION NUMBER: US/09/540,210B

PRIOR FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 08/972,899
PRIOR FILING DATE: November 18, 1997
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR FILING DATE: February 27, 1995
PRIOR APPLICATION NUMBER: 08/772,922
PRIOR FILING DATE: September 27, 1996
PRIOR APPLICATION NUMBER: 60/005,526
PRIOR FILING DATE: September 29, 1995
PRIOR APPLICATION NUMBER: 08/824,029
PRIOR FILING DATE: March 25, 1997
PRIOR APPLICATION NUMBER: 60/014,010
PRIOR FILING DATE: March 25, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/903,555
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/862,178
PRIOR FILING DATE: May 22, 1997
PRIOR APPLICATION NUMBER: 60/018,217
PRIOR FILING DATE: May 23, 1996
PRIOR APPLICATION NUMBER: 08/881,589
PRIOR FILING DATE: June 24, 1997
PRIOR APPLICATION NUMBER: 60/021,275
PRIOR FILING DATE: June 25, 1996
PRIOR APPLICATION NUMBER: 08/903,802
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/905,881
PRIOR FILING DATE: August 1, 1997
PRIOR APPLICATION NUMBER: 60/025,204
PRIOR FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 08/903,471
PRIOR FILING DATE: July 30, 1997
PRIOR APPLICATION NUMBER: 60/025,478
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/903,556
PRIOR FILING DATE: July 31, 1997

PRIOR APPLICATION NUMBER: 60/025,217
PRIOR FILING DATE: August 22, 1996
PRIOR APPLICATION NUMBER: 08/937,142
PRIOR FILING DATE: September 23, 1997
PRIOR APPLICATION NUMBER: 60/026,598
PRIOR FILING DATE: September 24, 1996
PRIOR APPLICATION NUMBER: 08/960,746
PRIOR FILING DATE: October 29, 1997
PRIOR APPLICATION NUMBER: 60/030,144
PRIOR FILING DATE: October 30, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/755,524
PRIOR FILING DATE: November 22, 1996
PRIOR APPLICATION NUMBER: 60/007,495
PRIOR FILING DATE: November 22, 1995
PRIOR APPLICATION NUMBER: 09/021,031
PRIOR FILING DATE: February 10, 1998
PRIOR APPLICATION NUMBER: 60/039,325
PRIOR FILING DATE: February 13, 1997
PRIOR APPLICATION NUMBER: 09/035,172
PRIOR FILING DATE: March 4, 1998
PRIOR APPLICATION NUMBER: 60/040,431
PRIOR FILING DATE: March 5, 1997
PRIOR APPLICATION NUMBER: 09/041,894
PRIOR FILING DATE: March 12, 1998
PRIOR APPLICATION NUMBER: 60/040,199
PRIOR FILING DATE: March 14, 1997
PRIOR APPLICATION NUMBER: 09/050,817
PRIOR FILING DATE: March 30, 1998
PRIOR APPLICATION NUMBER: 60/043,792
PRIOR FILING DATE: April 11, 1997
PRIOR APPLICATION NUMBER: 09/074,999
PRIOR FILING DATE: May 8, 1998
PRIOR APPLICATION NUMBER: 60/048,431
PRIOR FILING DATE: May 29, 1997
PRIOR APPLICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL Program
SEQ ID NO 15021
LENGTH: 277
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID NO: hu00004808
US-09-540-210B-15021

Query Match 1.3%: Score 36.4; DB 5; Length 277;
Best Local Similarity 50.6%: Pred. No. 4.5;
Matches 88; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 878 caggcaatcgtgtaggaatttttagtgacaatacaaaaaataatgagcgagcta 937
Db 187 CTGCCAAGTTGGTCTCTTTTACGTAATAATGTCAGATGCAAAATGCTGCACCTTA 128
Qy 938 tttagcctccgtagttccctcagtgagataatgagccaccacttaatacaaatcgc 997
Db 127 TTCTCTTAATATATGAAATAGTGAAGATGACGATTTTAAATTTCTTCACTGACTTA 68
Qy 998 caataataagggggcgctatclatalagacgagacgacactccaatctt 1051
Db 67 GCTGACATGACTTCTGCTAAGCGGCTCTTGAACATGACTTCAACTCAACTT 14

Submitted (12-JUN-1999) Genoscope - Centre National de Séquençage
BP 191 91008 EVRY cedex - FRANCE (E-mail : segreffgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fritfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Oosawa and
Aaron Mammeter in Pierlet de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial

Best Local Similarity 14.6%: Pred. No. 5.5:
Matches 51: Conservative 161: Mismatches 137: Indels 0: Gaps 0:

Oy 365 atacaatagctcgttaacttgaanaataactgtgtgcagaccattacatcgagta 424
||| : : : | : ||| : : : | :
Db 749 ATAMWTADATWMTKKAATDADAKRAAGRRKRDARKTADGGRARRRRRMAAGKRA 808
Oy 425 atcccaatgacgctgttaataaataagagagcgagcccttcacgtcctcaaatctt 484
:
Db 809 RAGARRARRRAADDDAWAAAAAAAWTTTRDWMDDMDTWTWDDDTTAA 868
Oy 465 acaataacataatcatgtgtgtcgagattatgaagaactcttccttcacgagag 544
:
Db 869 WMDDRARRRRRRRRRRRRARRAADDTPTKDRADADTTDDTKTKTTTDDDDMD 928
Oy 545 gacgcatagtagcagcaataacttgtgtgtgcagagacatgctgttctctta 604
:
Db 929 KAKRRMNAKADGAMKWDRAADMAATAKDDGKWKMGGRGKRGKDKRMKGTG 988
Oy 605 tggacaacatcgtattcaactaataacagcagaaagtgctctctctgtcgaga 664
:
Db 969 KDDDDMDTWTTRDWMWMTTKKMDWDDGGRGRTKRWGAMKRWADAMADDTDGKD 1048
Oy 665 cgagcaatcttgcagagataaactgcagctctctcttcaataa 713
:
Db 1049 TTTADKDKRTDTTKRDGDMDKRDKKRDKKGDGDKTKKDATWDDD 1097

RESULT 8
LOCUS BF298817
DEFINITION 021PbG02 Pb cDNA #20, Charles Yowell and Jane Carlton Plasmodium
berghel cDNA 5', mRNA sequence.
ACCESSION BF298817
VERSION BF298817.1 GI:13952043
KEYWORDS EST.
SOURCE Plasmodium berghel.
ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 667)
AUTHORS Carlton, J.M.-R. and Dame, J.B.
TITLE The plasmodium vivax and P. berghel gene sequence tag projects
JOURNAL Parasitol. Today 16 (10), 409 (2000)
COMMENT Contact: Dame JB
Department of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611-0880, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.vetmed.ufl.edu
Seq primer: 73.
FEATURES
source
1..667
Location/Qualifiers
/organism="Plasmodium berghel"
/strain="ANKA clone 15cyl (clone of the ANKA 8417 HP clone
)"
/db_xref="taxon:5621"
/clone_1lb="Pb cDNA #20, Charles Yowell and Jane Carlton"
/dev_stage="asynchronous blood stage"
/lab_host="Swiss white mice"
/note="Vector: pBluescript II vector DNA, excised from
lambda ZAP II.; Site 1: EcoRI, Site 2: XhoI. Total RNA was
extracted from asynchronous blood stage forms of the
cloned ANKA isolate of P. berghel grown in laboratory
Swiss white mice. Contaminating host white cells had
previously been removed using a novel biomagnetic bead
protocol (J. Carlton et al., manuscript in preparation).
PolyA+ RNA was extracted and reverse transcribed using an
oligo dt-XhoI primer. Second strand cDNA was prepared
using RNase H and DNA polymerase I. EcoR I adaptors were
ligated to the cDNA, and it was digested with XhoI.
Fragments were size selected, and those between 1-5 kb
ligated into EcoRI /XhoI digested vector."

BASE COUNT 339 a 49 c 70 g 209 t
ORIGIN

Query Match 1.4%: Score 41.2: DB 11: Length 667:
Best Local Similarity 48.3%: Pred. No. 5.7:
Matches 115: Conservative 0: Mismatches 123: Indels 0: Gaps 0:

Oy 263 atacacaaagaaggtatttlttgcaaaaatctccaccctgaaatgtgtgtgga 322
||| : : : | : ||| : : : | :
Db 149 ATGAAACAAATATGATATGAAATGCAAGCATATTAACGTAAAGCGCAATGATA 208
Oy 323 ttggtatcgagatcccaatctcctaccggtgagatcgatatacaataggtctgtaa 382
||| : : : | : ||| : : : | :
Db 209 TTTTATTAACAGTTATATTAATGTAATAATAGTAATAGTAATAGTATGATGANA 268
Oy 383 tcttgaataataactgtgtgcagacattacacgtaactcctaagcagctgtta 442
:
Db 269 AATAGCAAAAAATATATAGTACAAACATAGAAATATATATATATATATATAG 328
Oy 443 ataaataagagagcgagccatcatgctcaaatcttaccataatacatca 500
||| : : : | : ||| : : : | :
Db 329 ATTAACCAAT 386

RESULT 9
LOCUS CNS017DP/c
DEFINITION Drosophila melanogaster genome survey sequence Sp6 end of BAC
BACN17B14 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL107911.1 GI:5628215
VERSION AL107911.1 GI:5628215
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyceta;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage;
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk/. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billard at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES
source
1..1101
Location/Qualifiers
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone_1lb="DrosBAC"
/clone="BACN17B14"
/note="end: Sp6"

BASE COUNT 319 a 155 c 125 g 285 t 217 others
ORIGIN

Query Match 1.4%: Score 41: DB 13: Length 1101:
Best Local Similarity 33.9%: Pred. No. 7:
Matches 81: Conservative 49: Mismatches 109: Indels 0: Gaps 0:

Oy 2176 atgacgagcagacacacaccccttcattgaatcagtcagaccacacacat 2235
||| : : : | : ||| : : : | :
Db 896 ATMAAHACGSKHMAKACCTTTTWTWKMRGKATATAGAKATMGAYMAATTHACM 837

Oy	104	ctagaagaagtcgctatcaataaatttatttgcagggagacatcacatctcata	163
Db	699	CAAAATAAATGCTCCTCCATCCATTAATAATTATTAACCAAAAGAAATTATAGTCACCTTA	640
Oy	164	actgcctatcgcataaccctacgcctacatactgcgtatctctcaaaaaaaccctccaaatgaag	223
Db	639	AATTGAAATACCTTCATTTCCAGAAATTTCTGTATTAGATCAAAATTTCAATCAATAAAA	580
Oy	224	gagcgcgcgtccacaataacagatctaccctaaagcttllttgatacacaaaaaagaagattt	283
Db	579	AATTGGATATTTAAAGTTCCAGATATCAACGATTAAATTAAGTAAATGAATGAATTAATTT	520
Oy	284	atttgcaaaaaatctcaccccttgaag	310
Db	519	TAAAGAAGAAATAATTTCCTTAGAAA	493

RESULT	12
LOCUS	A0981798/c
DEFINITION	RPC1-23-303B16.TV RPC1-23 Mus musculus genomic clone RPC1-23-303B16
ACCESSION	A0981798
VERSION	A0981798
KEYWORDS	GI:6814099
SOURCE	house mouse.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 575)	Zhao, S., Niemman, M., Feldblyum, T., Malek, J., Shatsman, S., Akirnet, B., Levins, M., McGinn, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCT-23	Unpublished (1999)	Other_GSSS: RPCT-23-303B16.TJ

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPI-23. For BAC library availability, please contact Pieter de Jong (pieter@ed.jong.med.buffalo.edu). Clones may be purchased from BACpac Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac-ends/mouse/bac_end_intro.html
Plate: 303 row: B column: 16
Seq primer: 77
Class: BAC ends.

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FEATURES
source
Location/Qualifiers
1..575
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-303B16"
/clone_11b="RPCI-23"
/sex="female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site-1:
ECORI; Site-2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EORI and EORI Methylase. Size
selected DNA was cloned into the pBAC3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT
208 a 67 c 80 g 220 t
ORIGIN

```

Query Match

1.48; Score 40.4; DB 13; Length 575;

Best Local Similarity	43.3%	Pred. No. 9.1:	Matches 188:	Conservative 0:	Mismatches 246:	Indels 0:	Gaps 0:
OY	1295	tatttcaggagctactctttaa	ttcaatcgcagatattc	atccaaagcaatc	atccaaacaaaa	1354	
Db	500	TATATTAATTTGTTAAATGA	AAATGTATCTCAATGAT	AAACCTTTTCTTCAAAATCA	ATC	441	
OY	1355	caccgcaccccttactctc	agtaatgtgtttctat	gtatcgaagatcat	gtccagctta	1414	
Db	440	AAGGATATACATTTTGTG	GGTTTAAAAATTCATATTTAT	TGAGACTCAATTCATCACTTA	381		
OY	1415	cagtgaaatcgaatccaca	aaactgggggtgtgtt	cttctcttggaaat	gagacagttctga	1474	
Db	380	TTATTTAATATATATGCA	ATCAAAAGAGCTGATTTA	ATATACACCAAAAGATTA	TATATATTTTGA	321	
OY	1475	gtctgataaaaaatggg	ycaggaatctctgtc	tagcaatgacctctat	aacactgaaagcata	1534	
Db	320	TTTTTGAATTAATTAATTA	AAAGCTGATAGACACCTA	ATATTTTATGATTTGCAAG	GTAT	261	
OY	1535	ttgagtgaatccttcttc	atccatctcgaaaag	tggtgcgcagagatc	cttattgtggtag	1594	
Db	260	TTCTCTGTCCTTCAATAG	TTAGCAAAATATTAGCATTA	ATAATTTTATATAATTTGTA	CTACT	201	
OY	1595	agccacaataacagcaata	actaatacagacagata	ctgcagctacccctt	catcaatg	1654	
Db	200	AGCATTAATATGAATCG	ATATTATTTTTCAGTAC	AACTTTGTATATAAGTTA	CTACTAG	141	
OY	1655	atgtaaactctcactcat	cttgatgactatggaa	ttccctctatgaat	ccacagatctaa	1714	
Db	140	AACACTAATTTGATTTAA	AATTCCTGCAGATTAAT	TTCATATTAATAAAATTTCT	TTCATAC	81	
OY	1715	cccatgctctgtca	1728				
Db	80	TCTTACACTGCCA	67				
RESULT 13							
LOCUS	A2900612	487 bp	DNA	GSS	05-MAR-2001		
DEFINITION	RPci-24-150H6.TJ	RPci-24	Mus musculus genomic clone	RPci-24-150H6,			
KEYWORDS	A2900612						
VERSION	A2900612.1	GI:13219557					
ORGANISM	GSS.						
SOURCE	house mouse.						
REFERENCE	Mus musculus						
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
	1 (bases 1 to 487)						
	Zhao,S., Nlemaan,W., Malek,J., Shatsman,S., Akintel,B., Levins,M.,						
	Tsegaye,G., Geer,K., Krol,M., Shwartsbeyn,A., Gebregeorgis,E.,						
	Russell,D., de Jong,P. and Fraser,C.M.						
	Mouse BAC End Sequences from Library RPci-24						
	Unpublished (1999)						
	Other-GSS: RPci-24-150H6.TJ						
TITLE	Contact: Shaying Zhao						
JOURNAL	Department of Eukaryotic Genomics						
COMMENT	The Institute for Genomic Research						
	9712 Medical Center Dr., Rockville, MD 20850, USA						
	Tel: 301 838 0200						
	Fax: 301 838 0208						
	Email: szhao@ligr.org						
	Clones are derived from the mouse BAC library RPci-24. For BAC						
	library availability, please contact Pierer de Jong						
	(pdejong@mail.cho.org). Clones may be purchased from BACPAC						
	Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC						
	plate: 150 row: H column: 6						
	Seq primer: SP6						
	Class: BAC ends.						
FEATURES	Location/Qualifiers						
source	1..487						
	/organism="Mus musculus"						

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cloned in the BamHI site of pBSLTK+. See [4].
Genes are predicted from matches to other sequences. For more information about this sequence or the Paramesium Project, see <http://paramesium.cgm.cnr5.gif.fr>.
Location/Qualifiers

BASE COUNT	271 a	58 c	68 g	165 t
ORIGIN				

Query Match	1.4%	Score 40.2	DB 13	Length 562
Best Local Similarity	54.4%	Pred No. 10		
Matches 81	Conservative 0	Mismatches 66	Indels 0	Gaps 0
965 ataatgcccctccactttataaacatatcccaataataagg999cgctatctata 1024				

Qy	965	ataatggccctactactttaaataacatctgcacataataaga999gcgtactcta	1022
Db	187	ATAATAGCAATACACACGCAATACACATATACATATATATAACACACACATTAACACATTA	246
Qy	1025	tagacggacacagcaactccaaaattctgcgacccgcatgctatattttaaaga	1088
Db	247	ATTATACACACGCAATACACATATATATAGCAATTAACACATTAACCAATTAATAGTAATTATA	306
Qy	1085	attattgactactaatcttaactcaatc	1113

Db 307 ATAATACTATTATTTTAACTCAAT 335

RESULT	15
AA550487/c	
LOCUS	493 bp DNA
DEFINITION	GSS 05-DEC-2000
	1642m3 gmbpfHBB.1, G. Roman Reddy Plasmodium falciparum genomic clone 1642m, DNA sequence.
ACCESSION	AA550487
VERSION	AA550487.1 GI:2320739

MEDICINE
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 1 (bases 1 to 493)
 G55.
 malaria parasite P. falciparum.
 Plasmodium falciparum
 Eukaryota: Alveolata: Apicomplexa: Haemosporida: Plasmodium

ACKNOWLEDGEMENTS
AUTHORS
Dame, J.B., Arnot, D.E., Bouke, P., Chakrabarti, D., Christodoulou, Z., Coppel, R., Comman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinnerberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.V., Reddy, G.R., Rubio, J., Schuster, S.M., Su, X.-Z., Thompson, J.K., Vital, F., Wellens, T.E., and Werner, E.

TITLE
Current status of the *Plasmodium falciparum* genome project

JOURNAL
Mol. Biochem. Parasitol. 79, 1-12 (1996)

COMMENT
97001675

Contact: Dame, J.B.

Continued
Contact: Dr. James M. Dame, Department of Pathobiology, College of Veterinary Medicine, University of Florida, 2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel.: 352 392 4700
Tel.: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.vetmed.ufl.edu
See <http://www.vetmed.ufl.edu>
See <http://www.vetmed.ufl.edu>

```

class: Shotgun
source:
  Location/Qualifiers
    1..493
    /organism="Plasmodium falciparum"
    /db_xref="taxon:5833"
    /clone="1642m"
    /clone_1fb="cmbpFH3.1, G. Roman Reddy"

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//lab_host="E. coli XL1-Blue"
 //note="Vector: pBluescript SK(+): Genomic DNA, from
 asynchronous blood stage parasites of the cloned Honduran
 HB3 isolate cultured in vitro, was digested with mung bean
 nuclease in the presence of 30% formamide at 500C (Nericic
 K. D., Imberiski R. B., and McCutchan, T. F., 1988. Nucleic
 Acids Research 16:6883-6896). The ends of the fragments

Oy	2236	gagcgcttcacgaagaacacgtactccttaaaaattacttccgaaggagaatgc	2295
Db	836	BAYMACCTAAAYMRRRRAWIGTAKTTKAYAAATWDATKMGCACAAAAGADATTWTHAY	777
Oy	2296	tctcatctcaagaaggtctcttgctgcataaatagtggccttacagctatagac	2355
Db	776	TCCYTTTTTTAMATTTTTTTTTTTAATMGCAVTTTWTFHYTDNAHAAAAKAAGA W	717
Oy	2356	catacctgcaccattctctatccccaaaggagaagaatctaacctctcaaggagctcg	2414
Db	716	AMGAAMACCCTWCACAGKATATACAACBGBDMAAATASSCCATCAGAGGKKMATTCMC G	658
RESULT	10		
LOCUS	AZ529319/c		
DEFINITION	AZ529319	891 bp	DNA
ACCESSION	AZ529319		GSS
VERSION	AZ529319		03-NOV-2000
KEYWORDS	AZ529319.1	GI:11082075	
SOURCE	GSS.		
ORGANISM	Entamoeba histolytica.		
REFERENCE	Entamoeba histolytica.		
AUTHORS	Eukaryota: Entamoebidae; Entamoeba.		
TITLE	1 (bases 1 to 891)		
JOURNAL	Loftus,B., Van Aken,S. and Fraser,C.		
COMMENT	Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library Unpublished (2000) Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: entae@ligr.org Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library Seq primer: M13-Reverse Class: Shotgun High quality sequence start: 33 High quality sequence stop: 793. Location/Qualifiers 1..891		

BASE COUNT	272 a	148 c	68 g	403 t
ORIGIN				
Query Match		1.48	Score 40.6	DB 13
Best Local Similarity		46.18	Pred. No. 8.7	Length 891
Matches 136	Conservative	0	Mismatches 159	Indels 0
				Gaps 0

Oy 1068 tatcatttcataatgaataatgttgctaactgaactaataatggtaccagtaagc 1127
 ||| | | ||| ||| ||| | | | | |
 Db 776 TATAATAAAAAAGATATATATGTGCAGATAAATAAAGTTAAAGCATATTATAGTAA 717

[illegible]

```

/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/vector: phos1: Site_1: Bst I: Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole-genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999). "

```

Query Match	1.4%	score 40.6	DB 13	length 919
Best Local Similarity	49.8%	Pred. No. 8.7		
Matches 103	Conservative	0	Mismatches 104	Indels 0
				Gaps 0

ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

source
1..968
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACRIAN19"
/note="end : TET3"
BASE COUNT 249 a 280 c 60 g 197 t 182 others
ORIGIN

Query Match 1.5%, Score 43; DB 13; Length 968;
Best Local Similarity 42.5%, Pred. No. 2;
Matches 77; Conservative 16; Mismatches 88; Indels 0; Gaps 0;

Oy 903 tagtacaatcacaaaaattatgcgcgagcttaccgtcctgagttaccctagt 962
Db 551 TAGMWRTRAAATNATKAAAGGKATKKTCTTTTGGKKTATRTTNTTANNTATT 492
Oy 963 ggaatagccctactcttataacaataatgcgaataaaggagggcgctatccta 1022
Db 491 WTATATTTNTTNTTGTNTGTTTATATATATATATATATATATATATATATAT 432
Oy 1023 tatagacggaaccgaactccaaattctgcgcgacgcctgctatattttaaga 1082
Db 431 AATAATRAAGTAGATGMAGNAGCCVMATCTCTMCCCTCCCNATNCTCTCTGTTAGCT 372
Oy 1083 a 1083
Db 371 A 371

RESULT 6

AZ068468 538 bp DNA GSS 30-MAR-2000
LOCUS RPCI-23-420L3.TJ RPCI-23 Mus musculus genomic clone RPCI-23-420L3,
DEFINITION DNA sequence.
ACCESSION AZ068468
VERSION A2068468.1 GI:7359720
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 538)
Zhou,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akintet,
B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
CONTACT: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org

TITLE
JOURNAL
COMMENT
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@edj.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tcldb/Bac_ends/mouse/bac_end_intro.html
Plate: 420 row: L column: 3
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers

FEATURES

Location/Qualifiers

SOURCE

1..538
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-420L3"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; vector: pBAC3.6; Site_1: EcorI; Site_2: EcorI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcorI and EcorI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcorI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 173 a 82 c 121 g 162 t
ORIGIN

Query Match 1.4%, Score 41.6; DB 13; Length 538;
Best Local Similarity 59.2%, Pred. No. 4.4;
Matches 71; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Oy 804 taaaatgtagaacagctcttcagaagctctgagtgaggaagcaatgaactac 863
Db 415 TTAAGATTAAACTTAAGTCTCATATGCTTTTGGAGGTGCACTACAGAACTTC 474
Oy 864 tcgcctagatgtacaggaacatcgtagagatcttcttagtgacaaatacaaaaa 923
Db 475 TGCCCTAGTTTGCAGAAAGAAATATATGAGCTTCTTAGAACACAAATATACAGAAATA 534

RESULT 7

CNS0182P 1101 bp DNA GSS 26-JUL-1999
LOCUS CNS0182P
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL108811
VERSION AL108811.1 GI:5629115
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Plasmid Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage;
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage;
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web: www.genoscope.cns.fr
- Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP).
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

COMMENT

FEATURES
source
1..1101
Location/Qualifiers

/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN37D10"
/note="end : SP6"
BASE COUNT 274 a 268 c 128 g 73 t 358 others
ORIGIN

Query Match

1.4%, Score 41.4; DB 13; Length 1101;


```

RESULT 14
US-10-105-299-13644/c
: Sequence 13644, Application US/10105299
: GENERAL INFORMATION:
: APPLICANT: Rosen, et. al
: TITLE OF INVENTION: Human Secreted Proteins
: FILE REFERENCE: PS950
: CURRENT APPLICATION NUMBER: US/10/105, 299
: CURRENT FILING DATE: 2002-03-26
: NUMBER OF SEQ ID NOS: 15197
: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 13644
: LENGTH: 4205
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-105-299-13644

```

Query Match	1.2%	Score 35.4	DB 6	Length 4205
Best Local Similarity	59.4%	Pred. No. 16		
Matches 60	Conservative 0	Mismatches 41	Indels 0	Gaps 0

Qy 2177 tagcagggcagacacacacacacttctcatatgaaattcagtcagccctacaaccaactcaatg 2236
 || ||| | ||| ||||| | | | ||| | | |||
 Db 3761 TAACAGGAATGACATACAAAGTCTCTATTGCTTAACTGAATATATACACATAAATAAATA 3702

Oy 2237 agcgttacgcaaaaaaacacgtatcttctaanaattactca 2277
|| || || || || || || || || || || || || || ||
Db .3701 GGCACCTAACATATTAGAAAACATTTTCTTAATATATTTTA 3661

```

RESULT 15
US-10-105-299-2465/c
; Sequence 2465, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human secreted Proteins
; FILE REFERENCE: PS950
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ. ID NOS: 1519
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2465
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-2465

```

Query Match	1.2%	Score 35.2	DB 6	Length 1481
Best Local Similarity	52.8%	Pred. No. 14		
Matches 76; Conservative	0	Mismatches 68	Indels 0	Gaps 0

Qy 1323 agatttcatcaacycaatttacaacaacacctgcacccctactctcagtaatgg 1382

Db 405 AGCATTCAATAACGAAGTTTGGAGTAACATCCACGTTATCTTCCTTTCACATAATCA 346

Oy 1383 tttctatgtatcgaagatcaatgctcagcttaacgttaacatcattccacaaactg99gg 1442
 ||| ||| | ||||| | ||||| ||| |||
 Db 345 CGTTCCTCTTAAGCAGCATCTTAACAACAGCAGCAGTGAAGTGAATGTAATGAATTAAGACA 286

QY 1443 t g t t g t t c t c t t g q q a a t q q a c 1466

Db 285 TTTGATACACTAGAAACAGTGC 262

Search completed: April 24, 2002, 06:13:27
Job time: 3674 sec

```
Query Match 1.38: Score 38.2; DB 6; Length 9477;
Best Local Similarity 52.18; Pred. No. 4.2;
Matches 85: Conservative 0; Mismatches 78; Indels 0; Gaps 0;

OY 1304 gactactgttaatttcgcagatttcatacagcatttcacaacaaacacactgcac 1363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8408 GATAAATTGCAATCTTTAGCATTTCAATTAACGAAGTTTGGAGTACATCCACGTTT 8349

OY 1364 cccctactctcagtaagtgtttctatgatcgaagatcagtcacagcttacagtgatc 1423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8348 ATCTTCCTTTCACATAACACGCTCCCTGTTAGCACATCATACACACACAGTGAAGT 8289

OY 1424 gattcacacaactcgggggtgtgttctctcttggaatgagc 1466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8288 GAATGATGAATAAGACATTTTGATACACTAGAAACAGTGC 8246

RESULT 9
US-10-105-299-13242/c
: Sequence 13242, Application US/10105299
: GENERAL INFORMATION:
: APPLICANT: Rosen, et. al
: TITLE OF INVENTION: Human Secreted Proteins
: FILE REFERENCE: P5950
: CURRENT APPLICATION NUMBER: US/10/105,299
: CURRENT FILING DATE: 2002-03-26
: NUMBER OF SEQ ID NOS: 15197
: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 13242
: LENGTH: 9496
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-105-299-13242

Query Match 1.38: Score 38.2; DB 6; Length 9496;
Best Local Similarity 52.18; Pred. No. 4.2;
Matches 85: Conservative 0; Mismatches 78; Indels 0; Gaps 0;

OY 1304 gactactgttaatttcgcagatttcatacagcatttcacaacaaacacactgcac 1363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8427 GATAAATTGCAATCTTTAGCATTTCAATTAACGAAGTTTGGAGTACATCCACGTTT 8368

OY 1364 cccctactctcagtaagtgtttctatgatcgaagatcagtcacagcttacagtgatc 1423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8367 ATCTTCCTTTCACATAACACGCTCCCTGTTAGCACATCATACACACAGTGAAGT 8308

OY 1424 gattcacacaactcgggggtgtgttctctcttggaatgagc 1466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8307 GAATGATGAATAAGACATTTTGATACACTAGAAACAGTGC 8265

RESULT 10
US-09-789-189-553
: Sequence 553, Application US/09789189
: GENERAL INFORMATION:
: APPLICANT: Lelias, Jean-Michel
: TITLE OF INVENTION: Human Polynucleotides and Polypeptides
: FILE REFERENCE: 25436/1720
: CURRENT APPLICATION NUMBER: US/09/789,189
: CURRENT FILING DATE: 2001-02-20
: PRIOR APPLICATION NUMBER: 60/183452
: PRIOR FILING DATE: 2000-02-18
: NUMBER OF SEQ ID NOS: 2005
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 553
: LENGTH: 262
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-789-189-553
```

```
Query Match 1.38: Score 37.4; DB 5; Length 262;
Best Local Similarity 57.18; Pred. No. 2.5;
Matches 68: Conservative 0; Mismatches 51; Indels 0; Gaps 0;

OY 123 aataaatttggttgacagagagacactcacatctcactacatcgtcatctcgataacct 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 54 aaaaaatttccttactactacatcacatcacatcacatcacatcacatcacatcacatcac 113

OY 183 acgtacatactggtcttctacaaaaaacctcccaatgaaggagctgctgcacataa 241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 114 actatcactttataatctttaaaaaaatlccatcaaaaaatcactcctcaaaaaa 172

RESULT 11
US-09-828-523A-19/c
: Sequence 19, Application US/09828523A
: GENERAL INFORMATION:
: APPLICANT: The Pharmacia & Upjohn Company
: TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
: FILE REFERENCE: 268,62120101
: CURRENT APPLICATION NUMBER: US/09/828,523A
: CURRENT FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: 60/266,327
: PRIOR FILING DATE: 2000-04-06
: NUMBER OF SEQ ID NOS: 99
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 19
: LENGTH: 912
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
US-09-828-523A-19

Query Match 1.38: Score 36.6; DB 5; Length 912;
Best Local Similarity 51.58; Pred. No. 5.5;
Matches 84: Conservative 0; Mismatches 79; Indels 0; Gaps 0;

OY 330 tgcgagtcaccaatctctcactacgctgagagatcgtgatacaatagtcgtacattga 389
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 201 TGCAATGCCACTTTTCTTAAGATGATTCCTTGTTCCATCAACTCTACAATTTAGG 142

OY 390 aataaattctgttcgagaccatttactcgatgaatctcattcagctgttaataaat 449
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 141 CAATAACACTGCTGTAGATTATCTACACAAATATCCATGCTCTTAACATTTGAT 82

OY 450 aagaagaagcgagccattcgtcctcaaatcttactaaat 492
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 81 AACCAAGATTACTCTGCGCCAGATAAAGCTGTTACACTAAT 39

RESULT 12
US-09-828-523A-85/c
: Sequence 85, Application US/09828523A
: GENERAL INFORMATION:
: APPLICANT: The Pharmacia & Upjohn Company
: TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
: FILE REFERENCE: 268,62120101
: CURRENT APPLICATION NUMBER: US/09/828,523A
: CURRENT FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: 60/266,327
: PRIOR FILING DATE: 2000-04-06
: NUMBER OF SEQ ID NOS: 99
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 85
: LENGTH: 936
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Nucleotide sequence of S. aureus coding region cloned for expr
US-09-828-523A-85
```

```
FILE REFERENCE: 7969-086-999
CURRENT APPLICATION NUMBER: US/09/612,402A
CURRENT FILING DATE: 2002-03-29
PRIORITY FILING DATE: 1997-10-02
PRIORITY FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1515
TYPE: DNA
ORGANISM: Chlamydia sp.
US-09-612-402A-22
```

```
Query Match          1.7%: Score 48.4; DB 5; Length 1515;
Best Local Similarity 56.7%: Pred. No. 0.0092;
Matches 110; Conservative 0; Mismatches 81; Indels 3; Gaps 1;
```

```
QY 896 tcttttttagtgcacatacaaaaaattatgctgagctatttaccgtcctgtagta 955
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1007 ttctcttagtagcaatgtagctgtggaagggagctatttaccgcaaaagctct 1066
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 956 cccctagtgtgataatgcccctactactttataacaacatcgccataataagggggagc 1015
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1067 cggctgtcctaactgtgcccctgtacaaatttctaaggaatcgcataatgat--ggctgag 1123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1016 ctatctatagacggaacccaactccaattcttcgacgcgcctgtctatttt 1075
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1124 cgatttatttaggaagaatctggaagagccagttatctcgtctatgtagagatatattt 1183
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1076 ttaatgaaataatt 1089
      ||| ||| ||| |||
DB 1184 tcgatgggaatctt 1197
      ||| ||| ||| |||
```

RESULT 3

```
US-09-612-402A-1
Sequence 1, Application US/09612402A
GENERAL INFORMATION:
APPLICANT: Jackson, W. James
APPLICANT: Pace, John
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
FILE REFERENCE: 7969-086-999
CURRENT APPLICATION NUMBER: US/09/612,402A
CURRENT FILING DATE: 2002-03-29
PRIORITY FILING DATE: 1997-10-02
PRIORITY FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 4435
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant Expression Vector
NAME/KEY: CDS
LOCATION: (382)-(3417)
OTHER INFORMATION:
US-09-612-402A-1
```

```
Query Match          1.7%: Score 48.4; DB 5; Length 4435;
Best Local Similarity 56.7%: Pred. No. 0.012;
Matches 110; Conservative 0; Mismatches 81; Indels 3; Gaps 1;
```

```
QY 896 tcttttttagtgcacatacaaaaaattatgctgagctatttaccgtcctgtagta 955
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1472 ttctcttagtagcaatgtagctgtggaagggagctatttaccgcaaaagctct 1531
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 956 cccctagtgtgataatgcccctactactttataacaacatcgccataataagggggagc 1015
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1532 cggctgtcctaactgtgcccctgtacaaatttctaaggaatcgcataatgat--ggctgag 1588
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
QY 1016 ctatctatagacggaacccaactccaattcttcgacgcgcctgtctatttt 1075
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1589 cgatttatttaggaagaatctggaagagccagttatctcgtctatgtagagatatattt 1648
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1076 ttaatgaaataatt 1089
      ||| ||| ||| |||
DB 1649 tcgatgggaatctt 1662
      ||| ||| ||| |||
```

RESULT 4

```
US-09-612-402A-24
Sequence 24, Application US/09612402A
GENERAL INFORMATION:
APPLICANT: Jackson, W. James
APPLICANT: Pace, John
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
FILE REFERENCE: 7969-086-999
CURRENT APPLICATION NUMBER: US/09/612,402A
CURRENT FILING DATE: 2002-03-29
PRIORITY FILING DATE: 1997-10-02
PRIORITY FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 3324
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant Expression Vec
US-09-612-402A-24
```

```
Query Match          1.6%: Score 45.2; DB 5; Length 3324;
Best Local Similarity 55.7%: Pred. No. 0.067;
Matches 108; Conservative 0; Mismatches 83; Indels 3; Gaps 1;
```

```
QY 896 tcttttttagtgcacatacaaaaaattatgctgagctatttaccgtcctgtagta 955
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1094 ttctcttagtagcaatgtagctgtggaagggagctatttaccgcaaaagctct 1153
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 956 cccctagtgtgataatgcccctactactttataacaacatcgccataataagggggagc 1015
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1154 cggctgtcctaactgtgcccctgtacaaatttctaaggaatcgcataatgat--ggctgag 1210
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1016 ctatctatagacggaacccaactccaattcttcgacgcgcctgtctatttt 1075
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1211 cgatttatttaggaagaatctggaagagccagttatctcgtctatgtagagatatattt 1270
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1076 ttaatgaaataatt 1089
      ||| ||| ||| |||
DB 1271 tcgatgggaatctt 1284
      ||| ||| ||| |||
```

RESULT 5

```
US-09-612-402A-23
Sequence 23, Application US/09612402A
GENERAL INFORMATION:
APPLICANT: Jackson, W. James
APPLICANT: Pace, John
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
FILE REFERENCE: 7969-086-999
CURRENT APPLICATION NUMBER: US/09/612,402A
CURRENT FILING DATE: 2002-03-29
PRIORITY FILING DATE: 1997-10-02
PRIORITY FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 3354
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
```

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: ZIP: CA 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/602,737
: FILING DATE: 21-FEB-1996
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Marcus-Wyner, Lynn
: REGISTRATION NUMBER: 34,869
: REFERENCE/DOCKET NUMBER: 130-4080
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-354-3588
: TELEFAX: 415-857-1125
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3513 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: cDNA
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Bacillus thuringiensis
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..3513
: US-08-602-737-3

```

RESULT 15
US-09-001-982-3
Sequence 3, Application US/09001982
Patent No. 6204246
GENERAL INFORMATION:
APPLICANT: Bosch, Hendrick J.
APPLICANT: Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6204246artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```

1  APPLICATION NUMBER:  US/09/001,982
2  FILING DATE:
3  CLASSIFICATION:
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER:  US 08/602,737
6  FILING DATE:  21-FEB-1996
7  ATTORNEY/AGENT INFORMATION:
8  NAME:  Meigs, J. Timothy
9  REGISTRATION NUMBER:  38,241
10 REFERENCE/DOCKET NUMBER:  130-4080/PCT/CIP
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE:  919-541-8587
13 TELEFAX:  919-541-8689
14 INFORMATION FOR SEQ ID NO:  3:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH:  3513 base pairs
17 TYPE:  nucleic acid
18 STRANDEDNESS:  single
19 TOPOLOGY:  unknown
20 MOLECULE TYPE:  CDNA
21 HYPOTHETICAL:  NO
22 ANTI-SENSE:  NO
23 ORIGINAL SOURCE:
24 ORGANISM:  Bacillus thuringiensis
25 FEATURE:
26 NAME/KEY:  CDS
27 LOCATION:  1..3513
28 US-09-001-982-3

```

Query Match	Similarity	1.2%	Score 35.4	DB 4	Length 3513
Best Local	Similarity	55.2%	Pred. No. 2.8		
Matches	91	Conservative	0	Mismatches	71
				Indels	3
				Gaps	1
QY	349	accgcygagatgcgtgatacaatagtgccgtgaatccttgaaataatcgtgtgcga	408		
Db	1639	accatggaatattggggagagcttaacatctagaaacattagcttaaccattttgtaatt	1698		
QY	409	ccattacatcgagtaatccttaatgcagctgtgtataataataaggaagcgagcatt	468		
Db	1699	ccttttttctat--tttagggcttaatccagattatatttagaattgctgaagaaccttctatt	1755		
QY	469	catgtctaaatccttataataatcataatcatgatgtgtcga	513		
Db	1756	cctgttgctgacactttattatagataaaattgcaacttattcttgaca	1800		

Search completed: April 24, 2002, 06:12:08
Job time: 3760 sec

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Db      1639  ACCATGCAATTTGGGAGAGACTTAACATCTAGACACTTACTTACCAATTTAGTAAAT 1698
Oy      409  ccattacatcgagtaatccccaatgtagctgttataaataagaagaagcgagccatt 468
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1699  CCTTTTCAT---TTAGGCGTAATTCACATATATAATTAAGTAAGCTGGAAGACTTCTCATTT 1755
Oy      469  catctcaaatctctacataatcatcatcatgtagtgcgcga 513
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1756  CGTGTGCTGAGCCTTATATAGATATAAATTGCACTTATTCTAGCA 1800

RESULT 11
US-08-278-685-3
: Sequence 3, Application US/08278685
: Patent No. 5468483
: GENERAL INFORMATION:
: APPLICANT: Thompson, Mark
: APPLICANT: Gaetner, Frank H.
: TITLE OF INVENTION: No. 5468483el Bacillus thuringiensis Isolate
: TITLE OF INVENTION: Having Anti-Protozoan Activity
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Roman Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: FL
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/278.685
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/654,166
: FILING DATE: 12-FEB-1991
: APPLICATION NUMBER: US 08/091,527
: FILING DATE: 12-AUG-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Saliwanchik, Roman
: REGISTRATION NUMBER: 21,023
: REFERENCE/DOCKET NUMBER: 07/654,166
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 904-375-8100
: TELEFAX: 904-372-5800
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3513 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..3513
: US-08-278-685-3

Query Match 1.2%; Score 35.4; DB 1; Length 3513;
Best Local Similarity 55.2%; Pred. No. 2.8;
Matches 91; Conservative 0; Mismatches 71; Indels 3; Gaps 1

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Query Match	Similarity	1.2%	Score	35.4	DB	1	length	3513
Best Local	Similarity	55.2%	Pred	No. 2	8			
Matches	91	Conservative	0	Mismatches	71	Indels	3	Gaps
QY	349	accgctgagattcgtatcaataataggtccgtatctcttgaataataacttctgcaga	408					
DB	1639	accatggaattggcgacagccttaacatttagaaccttttagcatttttagtaatt	1698					
QY	409	ccatttaccagatgaatcctaattgcctctgttaataaataagaaagcgagacatt	468					
DB	1699	cccttttttct---tttagggcttaattccagattattatttagaattactcttaagaacacttccattt	1755					

OY	1460	atgagcagcgttcctgagttgctctaaataatggcgaggaattctgcctagcaatgcctcta	1519
Db	943	ATTGAGGTGGAGTCATACCTTGTTTAAATGTCACAGACGTACTCTTGACACACGACGAG	884
OY	1520	taacacccgaagacatatlgaattgaactcttcctccatcttcgaaagtggtgcctgaattc	1579
Db	883	TAAATATGTTGATTAATCCTTAATTAATTCATAAGTTGTCTAATTAATGAGTATATCTCG	824
OY	1580	cttatctggtgttagagccctaacaaataaagaacatacactatcacagatagctgaagta	1639
Db	823	GTTTTCGATACCTAAATCTCTTAAAGACATTTCTTAATCTTCATCATCATTAATGACAA	764
OY	1640	cccttcattaaatgtagtataaacctccatcaactcattgatagctatggaattctccattg	1699
Db	763	TTTCTCTTCATATTTTGGACATATAACATCACTCCAGACGCTCTCTCCGCTGCATATT	704
OY	1700	aatccacagatctaacccacagctctgycatcacaaagcctatgcctatct	1746
Db	703	CACGAATCGCTTTTACTTTATCATATATCATCATCACCAATTTTCATCT	657

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1  RESULT 2
2  US-09-273-613-3/C
3  ; Sequence 3, Application US/09273613
4  ; Patent No. 6203800
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Burnham, Martin K.R.
7  ; APPLICANT: Lonetto, Michael A.
8  ; APPLICANT: Warren, Patrick V.
9  ; TITLE OF INVENTION: NOVEL Gbpa
10 ; NUMBER OF SEQUENCES: 7
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: Dechert Price & Rhoads
13 ; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
14 ; CITY: Philadelphia
15 ; STATE: PA
16 ; COUNTRY: US
17 ; ZIP: 19103
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Diskette
20 ; COMPUTER: IBM Compatible
21 ; OPERATING SYSTEM: DOS
22 ; SOFTWARE: FastSEQ for Windows Version 2.0
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/09/273,613
25 ; FILING DATE:
26 ; CLASSIFICATION:
27 ; PRIORITY APPLICATION DATA:
28 ; APPLICATION NUMBER: 08/915,107
29 ; FILING DATE:
30 ; ATTORNEY/AGENT INFORMATION:
31 ; NAME: Dickinson, Todd Q
32 ; REGISTRATION NUMBER: 28,354
33 ; REFERENCE/DOCKET NUMBER: P50549-4
34 ; TELECOMMUNICATION INFORMATION:
35 ; TELEPHONE: 215-994-2252
36 ; TELEFAX: 215-994-2222
37 ; TELEX:
38 ; INFORMATION FOR SEQ ID NO: 3:
39 ; SEQUENCE CHARACTERISTICS:
40 ; LENGTH: 1122 base pairs
41 ; TYPE: nucleic acid
42 ; STRANDEDNESS: double
43 ; TOPOLOGY: linear
44 ; US-09-273-613-3

```

Query Match	1.48;	Score 40.6;	DB 4;	Length 1122;
Best Local Similarity	46.38;	Pred. No. 0.048;		
Matches 133;	Conservative	0;	Mismatches 154;	Indels 0;
Gaps				
Oy	1460	atggagcagttctyagttgctataaaatggtgycaggaaattctctgctagaatgcctcta	1519	

Db 943 ATTGAGGTGCAGTCATACCTGTTTAAATGTCGAAACGACGTACTCTTGCAACCCAGCAG 884
 QY 1520 taacactgaagcatalbtgataatccttcttccattctgaaaagtggtgctgagtc 1579
 Db 883 TAAATATGTTGGTATATCCATAATATTCATTAAGTTGTTTAAATGATCATTAATCTG 824
 QY 1580 cttaattgtggtagagcccaataacagcaataacatacagcaagctactgagcta 1639
 Db 823 GTTCTTGATACCTAAATCTTCTTAAGAACACTTTCCTTATCTTCATCATCATCACTTAATGAGAA 764
 QY 1640 ccttttcattaaagbalytaaaactctcactcatgagatgagactaagggaattctcctatg 1699
 Db 763 TTTCTTCTTAATTTTGGCACTAATAAACATCACTTCGACAGCTCTTTCGCGTGCATATT 704
 QY 1700 aatcacagatctaacccatcagctcgtcagcaagcctgcatct 1746
 Db 703 CAGCAATGCGTTTACTTTATTCATATCATCATCATCACTCACTTTCATCT 657

```

US-08-915-107-1
US-08-915-107-1/c
Sequence 1, Application US/08915107
Patent No. 5885805
GENERAL INFORMATION:
APPLICANT: Burnham, Martin K.R.
APPLICANT: Lonetto, Michael A.
APPLICANT: Warren, Patrick V.
TITLE OF INVENTION: NOVEL Gbpa
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915.107
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50549-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

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	Query Match	Similarity	Score	DB 2	Length	1125:	
Best Local	Similarity	46.3%	Pred. No. 0.048				
Matches	133:	Conservative	0:	Mismatches	154:	Indels	0:
						Gaps	0:
Qy	1460	atgagacgattcttgattgctataaaatggtgcaggaattctgtctagcaatgctctta	1519				
Db	943	ATTGAGTGCAGATCTACTACCTTGTTTAAAGTCCACAGACAGTACTCTTTCACACGACG	884				


```
RESULT 11
AAFS8254/C
ID AAF58254 standard: DNA: 936 BP.
XX
AC AAF58254:
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1875.
XX
KM Electron-transfer group: ETM; mismatch: genotyping;
KM gene expression: ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
WPI: 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface.
XX
PS Example 6: Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other:

Query Match 4.1%; Score 118.6; DB 22; Length 936;
Best Local Similarity 1.3%; Pred. No. 2.8e-23;
Matches 10; Conservative 480; Mismatches 299; Indels 0; Gaps 0:

OY 436 gctgttaataaataagaagagcgagccatcctgcctcaaatcttacaataatcat 495
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 789 GCWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 730

OY 496 aatcatgctgtgctcgattatagaagaacttctctatgctcgagagagccattagt 555
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 729 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 670

OY 556 accgctaataccttgtgtgagcagaatcagctctgtttctctcttcttgacaacatc 615
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 669 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 610

-OY 616 tctattcaaacataacagcagaaaagtgcgctatcctatgctgagcagcaattct 675
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 609 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 550

OY 676 tttagagtaataactgcagctctctcttatacaataacgctgtgtgcagagagagcg 735
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 549 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 490

OY 736 atcttccctctatctgtctctacaaggaatcggtgtaacatgctttctataacaat 795
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
DB 489 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 430

OY 796 cgtgctttaaaaaatagaaacagctcttcagaagctctgtagagagcaatlaaa 835
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 429 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 370

OY 856 gtaactactgcctagatgcttacagcgaatcggtgtagatctttttagagaacatc 915
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 369 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 310

OY 916 acaaaaaattatgtagcagatatttaacgtccgtgtagtaacctagtggaatagccct 975
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 309 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 250

OY 976 acctactttaaacaataatcgccaataaagggggagcgctatctatagacggaacc 1035
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 249 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 190

OY 1036 agcaactccaaaattctgctcgaccgcagctatctattttaaagaaatattgact 1095
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 189 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 130

OY 1096 aatgtaactaatgcaaatgtagccagtagtcagctcaatcctcctagaagaatgcaata 1155
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 129 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 70

OY 1156 acagtagcaagctcctcgtgtaaatctctatagagcagagagagccaaaattcaat 1215
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 69 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 10

OY 1216 ttctatgat 1224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 9 WWWWWWWWWWWW 1

RESULT 12
AAFS8257/C
ID AAF58257 standard: DNA: 936 BP.
XX
AC AAF58257:
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1954.
XX
KM Electron-transfer group: ETM; mismatch: genotyping;
KM gene expression: ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
WPI: 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface.
XX
PS Example 6: Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
```


OY	1253	ctgtctccctcaataaggaagcagctacaaacagggcctgtgatttttcaggagctacg	1312
Db	547895	ctccaatccttaattccaatgcgcaaccatcaaggagcatctattttcttcagcctata	547954
OY	1313	ttaatcttgagatctttcatcaacgcgaatttaaaaaaacactgaccccttactc	1372
Db	547955	tcccagaagctctcgactacgaataaattttcatagcagctcgaaaaataactctgac	548014
OY	1373	tcgattatggtttctctatgtatcgagaatcatctcagcttaacgaagtcatgatacgc	1432
Db	548015	ttcgcaatggtgtctctctctcatcgagatctggtcggaatgccaattcctaaagttaacc	548074
OY	1433	aaactcgggggtgtgtctctctctcttggaatgagacgttcctgagttgctataaagtgtg	1492
Db	548075	aaaaagaagatcatctcttaaattagggatgctggcgagttatgtacaacactgccaactcg	548134
OY	1493	caggaaatctctgtagcaatgctcctctataacactgaagcatattgatatgtatctttct	1552
Db	548135	agaactccatcaactagttgtagctccacaggtcatcatctaaactctgcatataaccctc	548194
OY	1553	ccattctcgaaaagcgtggtcgagatctccttatgtgtgggtgtagagccctacaataacagca	1612
Db	548195	ccctgcatcttagcacaagaagaaagcctctcactctgtgtgataccgtctctcaactcagtg	548254
OY	1613	ataactatcacgcagatactgcaagctactcctttcatatgaatgtaatgtaaaactctcaac	1672
Db	548255	ctcctctcacagagacataatcaactccaattactattatcagttcctcctcagcaactct	548312
OY	1673	ttgatgactatagggaatctctctctatgtaatcccaagatctcaacacagctctgtctac	1732
Db	548312	taaataggagaaaacccgagatcccatccacagcatataagatctctcgagcccttccaaa	548371
OY	1733	agccatctctatctattctctgagctagttgataacccgctcaagatcctgatatgtatg	1792
Db	548372	ttcaatctctttctttatcsgatgtataacgaagctcatatcaaccgataactcttcatc	548431
OY	1793	tttcgggaactaaatgtccctcctcatatgtgcaagaactttgactttgggctggg	1849
Db	548432	ctgaaagcttaaatgctgagctagatgaattacggtttatcaagatcttggtctccattatgg	548491
OY	1850	caaaaactcaagatccgaacacagcatctcttagcaacaatcacagatcccaaaaagcca	1909
Db	548492	-----tagagcagataacaacaacaataacgctctctatgagacggcaa	548556
OY	1910	atagatctcatagaacacttactactgacttgcttcctcgtctggtatgttcttagccga	1969
Db	548537	acaacctctacagagctctgtatgtagccaattggtactcccttagataagtaagtcactcg	548596
OY	1970	aacacagaatccctctatagcgaaatactaatgg-----gggaatatgctgttgcaa	2023
Db	548597	aatacaaggaagatcttactcagactccccccttagtgcgaatccttcatactatgtctctc	548656
OY	2024	cagaagctttaaataatgtagcagaacgacacactagatgatacctttctggggaatta	2083
Db	548657	tatttaagaagtataatcatcgaaactggtgtatcttgatatcgaaagcctctcttagaaattc	548716
OY	2084	caggaggaagctagcatgtatggttttaacaagatcctcgagaataatcatcctgtatctc	2143
Db	548717	aagggaatgcccagcgcctcttctgttcatcaataatagatcccggggctccaggaattcc	548776
OY	2144	ataatgcctctccggaatac-----tgggggagtatgtagcgagcgacacaaacct	2197
Db	548777	gtatccaactctcaaggtatcttccttaacaagatcctccgaaactctttatcatagaaaa	548833
OY	2198	ttctcatatgaattcagctagacactacacaacatcaatgacgttaccgcaaaaaacag	2257
Db	548837	ttctccttaggttttgacaggtttcttcacccgcgacataaagaatcggatcaagacaacag	548896
OY	2258	tatcttcaaaaattacatcagcagaagaaatgctcttctctatgtaagaagtcttct	2317
Db	548897	tctcggtctacaataacagctcttctcaactttatgtttagcttcgggtttccaaagagcct	548955

Oy	2318	tgcgactcaaaatttgcttggcgcttttaacagcgtatggagccataactctgcaccatttcata	2377
Db	548957	ltgcacaactccacagtggtltagcgfatatgcatatggaggccatcacctccaagcctaacc	549016
Oy	2378	cccaagaagaaaactcaacatctcaagggaagcttcgtagtcaaacyaiggagtgctg	2437
Db	549017	cctcaacctcaagaacaggca---gaagagacgtgttatagccatacataatgagcagcta	549073
Oy	2438	ttttttttagatcctccatatgaacccctttgatacaagcatatctcyaacgccctttt	2497
Db	549074	tcgcgtgtctcttcctccctvgcaac-----agaaatctcatcttcacacctcaagcccgttcg	549127
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Oy	2858	tctgtaatatctcatctcaatggggaattgctctcgattcta	2897
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XX	AA28711;		
AC	AA28711;		
XX			
DT	29-AUG-2000	(first entry)	
XX			
DE	C. pneumoniae CPN100626 open reading frame.		
XX			
KW	Antigen: anti-inflammatory; respiratory; antibacterial; anti-asthmatic;		
KM	anti-arteriosclerotic; vaccine; ds.		
XX			
OS	Chlamydia pneumoniae.		
XX			
PN	WO200024765-A2.		
XX			
PD	04-MAY-2000.		
XX			
PF	28-OCT-1999;	99WO-CA00992.	
XX			
PR	28-OCT-1998;	98US-0106034.	
PR	28-OCT-1998;	98US-0106039.	
PR	28-OCT-1998;	98US-0106042.	
PR	28-OCT-1998;	98US-0106044.	
PR	29-OCT-1998;	98US-0106072.	
PR	29-OCT-1998;	98US-0106073.	
PR	29-OCT-1998;	98US-0106074.	
PR	29-OCT-1998;	98US-0106087.	
PR	02-NOV-1998;	98US-0106587.	
PR	02-NOV-1998;	98US-0106588.	
PR	02-NOV-1998;	98US-0107034.	

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OY	2866	tatccaatggggaaattgctctgcgattctag	2898
Db	2902	tatccaatggggaaattgctctgcgattctag	2934
RESULT 5			
AAH56262	ID	AAH56262 standard; DNA; 2934 BP.	
XX	AC	AAH56262;	
XX	DT		
XX	DE	05-SEP-2001 (first entry)	
XX	XX	Chlamydia trachomatis pmpe gene.	
XX	KW	Chlamydia; vaccine; infection; fusion protein; antigen;	
KW	KW	pelvic inflammatory disease; trachoma; atherosclerosis; heart disease;	
KW	KW	acute respiratory tract infection; Cqpl; CtS29; OMCB;	
XX	XX	polymorphic membrane protein; pmp; thiol specific antioxidant; TSA; ds.	
OS	XX	Chlamydia trachomatis.	
PN	XX	WO200140474-A2.	
PD	XX	07-JUN-2001.	
PF	XX	04-DEC-2000; 2000WO-US32919.	
XX	PR	03-DEC-1999; 99US-0454684.	
PR	PR	19-APR-2000; 2000US-0558877.	
XX	PR	20-JUN-2000; 2000US-0598419.	
PA	XX	(CORI-) CORIXA CORP.	
PI	XX	Probst P, Bhatia A, Skeiky YAM, Fling SP, Scholler J;	
DR	XX	WPI: 2001-374831/39.	
PT	XX	Chlamydia polypeptides and fusion proteins useful for preventing pelvic	
PT	XX	inflammatory disease, trachoma, acute respiratory tract infections,	
PT	XX	atherosclerosis and heart disease -	

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REFERENCE
AUTHORS

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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscophora; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 298283)
Adams,M.D., Celisnker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
Amanalides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galie,R.F.,
Georg,R.A., Lewis,S.E., Richardson,S., Ashburner,M., Henderson,S.N.,
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Brandon,R.C., Rogers,Y.H., Blazer,R.G., Champe,M., Pfeiffer,B.D.,
Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor
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Zhang,F.N., Zhong,W., Zhou,X., Zhao,Q., Zheng,L., Zheng,X.H.,
Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,C.J.
The genome sequence of *Drosophila melanogaster*
Science 287 (5461), 2185-2195 (2000)
20196006

TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

2 (bases 1 to 298283)
Adams,M.D., Celisnker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced gi:7302138.

Location/Qualifiers

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TITLE Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
JOURNAL Pneumoniae AR39
Nucleic Acids Res. 28 (6), 1397-1406 (2000)
PUBMED 20150255
10684935
2 (bases 1 to 14482)
AUTHORS Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F.,
White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Ullrich, T.,
Barry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B.,
Bowman, C., Dodson, R., Gwin, M., Nelson, W., Deboy, R., Kolonay, J.,
McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
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ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM Chlamydomophila pneumoniae AR39.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

REFERENCE
AUTHORS Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Uterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouiri, H., Craven, B., Bowman, C., Dodson, R., Gwin, M., Nelson, W., Deboy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.

TITLE
JOURNAL Nucleic Acids Res. 28 (6), 1397-1406 (2000)

PUBMED
10684935

2 (bases 1 to 10236)

Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Uterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouiri, H., Craven, B., Bowman, C., Dodson, R., Gwin, M., Nelson, W., Deboy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.

Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
On Jun 1, 2000 this sequence version replaced gi:7189205.

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BASE COUNT 2874 a 1885 c 2466 g 3011 t

ORIGIN

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Matches 936; Conservative 0; Mismatches 1116; Indels 61; Gaps 8;

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Db 9074 GGTCCGACACCATTTATTAATCACTCGACACTTCAGAGAGCGCTCTCATCAATCTTTCT 9015

JOURNAL

Submitted (04-JUL-2000) to the DBJ/EMBL/GenBank databases.
Mutsunori Shirai, Yamaguchi University School of Medicine,
Department of Microbiology, 1-1-1 Minamikogushu, Ube, Yamaguchi
755-8505, Japan (E-mail:ms Shirai@po.cc.yamaguchi-u.ac.jp,
Tel:81-836-22-2227, Fax:81-836-22-2415)

COMMENT

On Sep 15, 2000 this sequence version replaced gi:6172290
gi:6172292 gi:6172294 gi:6172296 gi:6172326 gi:6172328 gi:6172330
gi:6172332 gi:6172334 gi:6172336 gi:6172338 gi:6172382 gi:6172384
gi:6172386 gi:6172388 gi:6172390 gi:6172392 gi:6172394 gi:6174666
gi:6174668 gi:6635174 gi:6635176 gi:6635178 gi:6635180 gi:8547433
gi:8547438 gi:8978640.
AB033782-AB033785, AB033800-AB033815: Submitted (25-Oct-1999)
AB038348-AB038349: Submitted (14-Feb-2000)
AB036079-AB036082: Submitted (18-Dec-2000).

FEATURES

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gene

CDS

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ACCESSION	AE001631 AE001363		
VERSION	AE001631.1 GI:4376750		
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SOURCE	Chlamydia pneumoniae CWL029.		
ORGANISM	Chlamydia pneumoniae CWL029		
REFERENCE	Bacteria: Chlamydiales: Chlamydiaceae: Chlamydia.		
AUTHORS	1 (bases 1 to 12083)		
TITLE	Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R. W., Olinger, L., Grimwood, J., Davis, R. W. and Stephens, R. S.		
JOURNAL	Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)		
MEDLINE	99206606		
PUBMED	10192388		
REFERENCE	2 (bases 1 to 12083)		
AUTHORS	Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L., Grimwood, J., Davis, R. W. and Stephens, R. S.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA		
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REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN
1	(bases 1 to 2934)	Probst, P., Bhalla, A., Skelley, Y.A., Fling, S.P. and Schollner, J.	Chlamydia sp.	Chlamydia sp.	875 a	645 c
2	Compounds and methods for treatment and diagnosis of Chlamydia infection	Patent: NO 0140474-A 183 07-JUN-2001:	Chlamydiales: Chlamydiaceae: Chlamydia.	Chlamydiales: Chlamydiaceae: Chlamydia.	645 c	575 g
3	Location/Qualifiers	1. 2934	Chlamydia sp.	Chlamydia sp.	575 g	839 t
4	Conservative	0; Mismatches	37; Indels	3; Gaps	1;	
5	Query Match	95.9%; Score 2777.8; DB 6; Length 2934;	Best Local Similarity	98.6%; Pred. No. 0;	Matches 2813;	Conservative
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7	106	acgaaagatcgctatcaataaattggtttgcacagagacaccccaatctcactaac	165			
8	145	ACGAAAGAGTCCCTATCAATTAATTAATTTGACAGGAGACCTCACATCTCACTAAC	204			
9	166	tgctatctgcataacctacagcacatcgcgtatctctcaaaaaaactcccatgaaga	225			
10	205	TGCTATCTGTAATACCTACGCTACATCTACGCTATTTCTCAAAAAAAGTCCCAATGAGGA	264			
11	226	gctgcgtcacataacagattaccctaagctttttgatacacaagaagatcttat	285			
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17	406	agaccatttatacagagtaactcaatgacgtgttgaataaataaagaagagcgagcc	465			
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